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Result
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Listing first 45 summaries
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                        Sequence 21228, A sequence 585, App sequence 585, App sequence 24743, A sequence 32625, A sequence 32625, A sequence 20039, A sequence 20039, A sequence 20039, A sequence 20237, Appl sequence 2169, A sequence 21, Appl sequence 21, Appl sequence 22, Appl sequence 21, Appl sequence 22, Appl sequence 28696, A sequence 28696, A sequence 28636, Apsequence 2184, Appl sequence 2184, Appl sequence 22184, Appl sequence 23184, Appl sequence 23184, Appl sequence 23184, Appl sequence 314, Appl sequence
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SEQUENCES RELATING D THERAPEUTICS	4; Length 164 63; Indels 27; Indels DGDVVLHALADAIL DGDVVLHALSDAIL DGDVLLHALSDAIL DGDVLHALSDAIL DGDVLHALSD	SEQUENCE:	0 P
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Patent No. 6559294
GEMERAL INFORMATION:
APPLICANT: Griffais, R.
APPLICANT: Or INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, frag
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, frag
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-99
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 585
LENGTH: 199
TYPE: NEW TABLES OF SEQ ID NOS: 6849
SEQ ID NO 585
LENGTH: 199
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Best Local :
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APPLICANT: Marc J.
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                                                                                                                                                                                                 Sequence 24743, Ap
Patent No. 6551795
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND ANNO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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mes 47; Conserv
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RESULT 6
US-09-252-991A-32625
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US-09-252-991A-26787
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                                                          Patent No. 6551795

GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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LENGTH: 560
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24743
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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UMBER: US 60/074,788
1998-02-18
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                                       GENERAL INFORMATION:
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TITLE OF INVENTION: NUCLETC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR TILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32082
LENGTH: 708
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                                                             Patent No.
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PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32625
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APPLICANT: Yang, Yan-Ping
                        APPLICANT:
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ORGANISM: Pseudomonas aeruginosa
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                                                             71, Application US/09206942
o. 6432669
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                 Loosmore, Sheena M.
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27.8%; Pred. No. 1;
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24.3%; Pred. No. 0.64;
ative 25; Mismatches
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US-09-252-991A-18149
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                        RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 18149
LENGTH: 220
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APPLICANT: Marc J.
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SEQ ID NO 71
LENGTH: 1477
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Best Local Similarity
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Patent No. 6551795
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: 1986-07-27
NUMBER: 0F SEQ ID NOS: 33142
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Best Local Similarity
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
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TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
TITLE OF INVENTION: Wolecular Weight Proteins
FILE REFERENCE: 1038-861 MIS:jb
CURRENT APPLICATION NUMBER: US/09/206,942
CURRENT FILING DATE: 1998-12-08
EARLIER APPLICATION NUMBER: 09/167,568
EARLIER APPLICATION NUMBER: 09/167,568
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                                                                                    152 DFVARDHQVVDRDLLQVQQAEQHVMPVDLAGLGVVGRMQGLFVAAASAVVLFRR 205
                                                                                                                            115 ANIAADLE-TDVDFINVKATTTE-----KLGFEGRKEGI---AVQAVVLIER 157
                                                                                                                                                                       103
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                                                                                                                                                                                                            55 LGDIGKHFPDTDPNFKGADSRVLLRHVYGIVKEKGYKLVNADVTIIAQAPKKLPHVPGMR 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
                                                                                                                                                                                                                                                                                                                                         43;
                                                                                                                                                                                                                                                     DVLQRDDADHL---AIFVDHHADTALLLLEVHQLGRQRRAFRHEIRLHAGLAEILLGQAA 102
                                                                                                                                                                                                                                                                                             DVHRFNDGDHIILGGVKIPYEKG-----LEAHSDG-----DVVLHA-LADAILGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKGYKLVNADVTIIAQAP 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKGGRAIVWGDI---ALIDGNINAQGSGDIAKTGGFVETSGHYLSIDSN-----AIVK 434
                                                                                                                                                                    LGQQARDLAHVHDPFDLVDVVAVDRQA-GVA--GGAQLLDDDLEFVVEVDAF--
                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                           9.48;
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                                                                                                                                                                                                                                                                                                                                       25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                           Score 75.5; DB Pred. No. 0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 77; DB 4; Length 1477; Pred. No. 4.2;
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                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                         67:
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                                                                                                                                                                                                                                                                                                                                         Indels 39;
                                                                                                                                                                                                                                                                                                                                         Gaps
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Sequence 20039, Application Patent No. 6551795

US/09252991A

GENERAL INFORMATION

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US-09-252-991A-23689
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US-09-252-991A-20039
                                                                                                                                                                                                                                                                                                SEQ ID NO 23689
LENGTH: 898
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23689, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                     Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                   09-252-991A-23689
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
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                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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LENGTH: 400
                                                                                                                                                                                                                        Local Similarity
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                                                                                                                      568 VGPGDEARVVMQNRNNDPRRAVGRRGHHAAAAGVLLVHRQGVEVDPVEHAESIAQAGLRP 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 PLAADLÁVGTVGQ-
                                          628 LAQLAVERRRAAPDLQSAGHDALVAAAGLDAILHHLPDTQQAGAGFLGGAPGLLV-----
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                                                                                                                                                              VGMGYDV-----HRFND-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDVGVDGEAHA----GQHPLLG----QHLLALQAHRFRQTQFGLDAARLAGGAVVVEDTLD
      IVKEKGYKLVNADV---TIIAQAPKMLPHVPGMRA-----NIAADLETDVDFINVK 131
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WENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
WENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marc J.
                                                                                                                                                                                                  9.1%; Score 73.5; Di
ilarity 22.7%; Pred. No. 5.3;
Conservative 22; Mismatches
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.4%; Score 75.5; DB 23.8%; Pred. No. 0.89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------DRRVLQRDVDLVVETVRHPALDLFATGTALVHRDM 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27; Mismatches
                                                                                DAILGAAALGDIGKHFPDTD----PNFKGADSRVLLRHVYG
                                                                                                                                                              -GDHIILGGVKIPYEKGLE-----AHSDGDVVLHA
                                                                                                                                                                                                                                           DB 4;
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Query Match
Best Local Similarity
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                                                                                          ORGANISM: Staphylococcus epidermidis US-09-134-001C-3855
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20237
                                                                                                                                                 SEQ ID NO 3855
LENGTH: 608
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3855, Ag
Patent No. 638037
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TITLE OF INVENTION: NUCLEIC ACID AND MAINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BEDIERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT PLILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PLILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER: OF SEQ ID NOS: 5674
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                               ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 1388
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o. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 DHIILGGVKIPYEKGL------EAHS-DGDVVLH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oh 9.1%;
| Similarity 24.2%;
| 36; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEDAFGGRRVAVHRGIFILHVBALQLAGVLEVADHHALDGDPLVHQRTFGAGALHLVDRS 332
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                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/091340010
              9.1%; Scc
21.7%; Pre
ative 22;
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                Score 73; DB Pred. No. 3.4; 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 73.5;
Pred. No. 1
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                                                       DB 4;
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                  33; Indels
                                                     Length 608
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                  46;
                Gaps
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Query Best Match	RESULT US-09-2 Seque Seque Paten GENER APPL TITL TITL TITL TITL TITL TITL TITL T	d da da	B &	Query Best Match	RESULT US-09-2 Seque Seque Paten GENER APPL TITL FILE CURR CURR CURR CURR CURR CURR CURR LEQ I SOFT SOFT SOFT SOFT TYP ORG	Qy da	5 A	0y
Query Match 9.0%; Score 72.5; DB 4; Length 267; Best Local Similarity 23.2%; Pred. No. 1.1; Matches 35; Conservative 21; Mismatches 44; Indels 51; Gaps	SULT 15 -09-252-991A-28466 -09-252-991A 28466, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION: APPLICANT: Marc J. Rubenfield et al. APPLICANT: Marc J. Rubenfield et al. TITLE OF INVENTION: AUGURIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: AUGURIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: AUGURIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: AUGURIC ACID AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 28466 CENCRIPH: 267 TYPE: PRT ORGANISM: Pseudomonas aeruginosa -09-252-991A-28466	58 IGKHFPDTDPNFKGADSRVLLRHVYGIVKEKGYKLVNADVTIIAQAPKMLPHVPGMRANI	3 RVGMGYDVHRFNDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGD	Query Match 9.1%; Score 73; DB 4; Length 1002; Best Local Similarity 24.8%; Pred. No. 7.3; Matches 33; Conservative 16; Mismatches 46; Indels 38; Gaps	RESULT 14 US-09-268-347-24 US-09-268-347-24 Sequence 24, Application US/09268347 Sequence 24, Application US/09268347 Patent NO. 635182 GENERAL INFORMATION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS PILE REFERENCE: 1038-860 CURRENT APPLICATION NUMBER: US/09/268,347 CURRENT FILING DATE: 1999-03-16 NUMBER OF SEQ ID NOS: 54 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 24 LENGTH: 1002 TYPE: PRT ORGANISM: Haemophilus influenzae US-09-268-347-24	Qy 99 IIAQAFKML 107 :: : : Db 485 VVRENEKLL 493	57 DIGKHFEDTDPNEKGADSRVLLRHVYGIVKEKGYKLVNADVT : : : : : : : : : :	18 HIILGGVKIPYEKGLEAHSDGDVVTHALADAILGAAALG
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Search completed: January 29, 2004, 15:57:06 Job time : 5.92742 secs

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1: /cgn2 6/prodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2 6/prodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2 6/prodata/1/pubpaa/US06 NEW_PUB.pep:*

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US-09-934-868-66
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US-10-189-762-585
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equence 17	equence 15	equence 14	equence 12	equence 18	equence 23	equence 22	equence 15	equence 12	equence 23	equence 15	equence 15	equence 14	equence 14	equence 13	equence 19	equence 13	equence 13	equence 19	Sequence 132	equence 14	equence 12	equence 12	equence 14	equence 12	e 11	equence 1:	equence 12	equence 13	equence 13
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                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Genes Involved in Isoprenoid Compounds Production FILE REFERENCE: CL1646 US NA CURRENT APPLICATION NUMBER: US/09/934,903 CURRENT FILING DATE: 2001-08-22 PRIOR APPLICATION NUMBER: 60/229,907 PRIOR FILING DATE: September 1, 2001 NUMBER OF SEQ ID NOS: 24 SOPTWARE: Microsoft Office 97 SEQ ID NO 10

LENGTH: 157
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Best Local Similarity
Matches 157; Conserv
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Patent No.
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APPLICANT: Odom, J. Martin
APPLICANT: Schenzle, Andreas J.
APPLICANT: No. US20020102690Atton,
APPLICANT: Tomb, Jean-Francois
                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Methylomonas 16a
FEATURE:
OTHER INFORMATION: Amino acid sequences encoded by ORF5
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o. US20020102690A1
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HFPDTDPNFKGADSRVLLRHVYGIVKEKGYKLVNADVTIIAQAPKMLPHVPGMRANIAAD 120
                                         MIRVGMGYDVHRFNDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGK
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Cheng, Qiong
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APPLICANT: Cheng, Qiong
APPLICANT: Dicosimo, De-
APPLICANT: Koffas, Matti
APPLICANT: Miller, Edway
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TITLE OF INVENTION: DENTIFIFYING MSTHANOTROPHIC BACTERIAL STRAIN
FILE REFERENCE: CL1596 US WA
CURRENT APPLICATION NUMBER: US/09/934,868
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Microsoft Office 97
SEQ ID NO 66
SOFTWARE: Mi
SEQ ID NO 14
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Patent No. US20020137190A1
                                                                     CURRENT APPLICATION NUMBER: US/09/941,947A
CURRENT FILING DATE: 2001-09-01
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 60
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                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Picataggio, Steve
APPLICANT: Rouviere, Pierre E.
TITLE OF INVERVIOU: CAROFENOID PRODUCTION FROM A SINGLE CARBON SOURCE
FILE REFERENCE: CL1903 US NA
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APPLICANT: Odom, James M
APPLICANT: Schenzle, Andre
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ORGANISM: Methylomonas 16a
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Miller, Edward S. Jr.
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DiCosimo, Deana J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Odom, J. Martin
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Pred. No. 3.5e-81;
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RESULT 5
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US-09-941-947A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 157;
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CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 60/299,058
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Louie, Gordon V.

APPLICANT: Buchanan, Sean Grant
APPLICANT: Gajiwala, Ketan S.

APPLICANT: Gajiwala, Ketan S.

APPLICANT: Sauder, J. Michael
TITLE OF INVENTION: CC-YSTALS AND STRUCTURES OF
TITLE OF INVENTION: 2C-YSTALS AND STRUCTURES OF
TITLE OF INVENTION: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: VARIANT
LOCATION: 1, 69, 108, 115
CTHER INFORMATION: Xaa = Selenomethionine
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                                                                                                                                                                                                                                                                                                                    63 LFPDTDXQYKNADSRGLLREAFDQVQBKGYKIGNVDITIIAQAPLXRPHIDAXRAKIAED
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nilarity 100.0%;
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Pred. No. 3.5e-81;
); Mismatches 0;
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Sequence 162, Applic Publication No. US20 GENERAL INFORMATION:

Application US/10259194A

APPLICANT: Lange, Markus B.

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PRIOR PILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,743
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 662
SOFTWARE: PatentList.pl version 3.0.4 (C) 20
SEQ ID NO 162
PRIOR FILING DATE: 223
; ORGANISM: Streptomyces avermitilis US-10-156-761-11502
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; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-259-194A-162
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                                                                                                APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR PILING DATE: 2001-08-02
NUMBER: OF 2501 DNOS: 15109
                                                            SEQ ID NO 11502
LENGTH: 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11502, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Best Local Similarity
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CURRENT FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                          TYPE: PRT
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Moughamer, Toum
Provart, Nicholas
wicke, Darrell
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                                                                                                                                                                                                                                                                                                                                                     IKEDA, HARUO
ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goff, Stephen A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glazebrook, Jane
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Briggs, Steven P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.7%; Score 360.5; DB 1
46.8%; Pred. No. 1.1e-31;
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RESULT 8
US-09-738-626-6421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         문
APPLICANT: HAYASHI, MIKIRO
APPLICANT: COCHIAL, KEIKO
APPLICANT: COCHIAL, KEIKO
APPLICANT: COCHIAL, KEIKO
APPLICANT: SENOH, AKCHHIKO
APPLICANT: SENOH, AKCHIRO
APPLICANT: SENOH, AKCHIRO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
FULE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,526
CURRENT PILLING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP99/377484
PRIOR PILLING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Rhodococcus erythropolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
US-10-128-713A-10
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CURRENT FILING DATE: 2002-04-22
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                 Sequence 6421, Application US/09738626
Publication No. US20020197605A1
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Matches
                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
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Best Local :
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                                                                                                                                                                                                                                                                                                                          APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bramucci,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Genes Involved in Isoprenoid Compound Production FILS REFERENCE: CL-1788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 19
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 IRVGMGYDVHRENDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 37.6 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGTGRPEWDGVSGARMLAEVRRLLEENQFTVGNAAVQVIGNRPKI-----GPRRDEAQKV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FPDTDPNFKGADSRVLLRHVYGIVKEKGYKLVNADVTIIAQAPKMLPHVPGMRANIAADL 121
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                                                                                                                                                                                                                                                                                                    MIZOGUCHI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/10128713A
No. US20030170847A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.7%; Score 247.5; DB 1
37.8%; Pred. No. 2.2e-19;
tive 24; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
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Pred. No. 1e-19;
3; Mismatches 67; Indels
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RESULT 10
US-10-289-762-585
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US-10-174-410-135
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                                                                                                                        Sequence 585, Applic
Publication No. US20
GENERAL INFORMATION:
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SOFTWARE: PatentIn ver. 3.
SEQ ID NO 6421
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SEQ ID NO 135
LENGTH: 32
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Best Local Similarity
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                  APPLICANT: Griffais, R. TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve TITLE OF INVENTION: and treatment of infection FILE REFERENCE: 9710-003-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/174,410
CURRENT FILING DATE: 2002-06-17
ERIOR APPLICATION NUMBER: 60/299,058
PRIOR FILING DATE: 2001-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sauder, J. Michael
TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF
TITLE OF INVENTION: 2C-METHLY-D-ERVITHITOL, 2,
FILE REFERENCE: 524982000300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Louie, Gordon V.
APPLICANT: Buchanan, Sean
APPLICANT: Gajiwala, Ketan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
CURRENT APPLICATION NUMBER: US/10/289,762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 160
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Gajiwala, Ketan S.
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                                                                                                                                                                       Application US/10289762
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32.9%; Pred. No. 1.3e
ative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       19.0%;
87.5%;
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Pred. No. 7e-10;
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RESULT 12
US-10-174-410-133
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US-10-174-410-129
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US-10-174-410-129
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Best Local Similarity 29.41

47; Conservative
                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 336
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 129
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
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NUMBER OF SEQ ID NOS:
SEQ ID NO 585
LENGTH: 199
                                                                                                                                                                                                                                    Sequence 133, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 129, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                             APPLICANT: Louie, Gordon V.
APPLICANT: Buchanan, Sean Grant
APPLICANT: Gajiwala, Ketan S.
APPLICANT: Gajiwala, Ketan S.
APPLICANT: Sauder, J. Michael
TITLB OF INVENTION: CRYSTALS AND STRUCTURES OF
TITLE OF INVENTION: 2C-METHLY-D-ERVTHRIFOL, 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Louie, Gordon V.
APPLICANT: Buchanan, Sean Grant
APPLICANT: Buchanan, Sean Grant
APPLICANT: Gajiwala, Ketan S.
APPLICANT: Gajiwala, Ketan S.
APPLICANT: Sauder, J. Michael
TITLE OF INVENTION: CCYSTALS AND STRUCTURES OF
TITLE OF INVENTION: 2C-MTHILY-D-ERYTHRITOL, 2,4-CYCLODIPHOSPHATE SYNTHASE MECPS
FILE REFERENCE: 524982000300
CURRENT APPLICATION NUMBER: US/10/174,410
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 60/299,058
PRIOR FILING DATE: 2001-06-18
CURRENT APPLICATION NUMBER: US/10/174,410
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 60/299,058
                                                                FILE REFERENCE: 524982000300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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Local
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                                                                                                                                                                                                                                                                                                                                                                                    40 VVLHALADAILGAAALGDIGKHPPDTDPNFKG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                17.7%;
1 Similarity 78.1%;
25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 DIGKHFPDTDPNFKG-ADSRVLLRHVYGIVKEKGYKLVNADVTIIAQAPKMLPHVPGMRA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 RTGIGQDSHRFLPESSTKPCILGGIIFDHCPGFQANSDGDIIFHAICNAISSVTNKIILG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 143; DB 15;
Pred. No. 8.9e-09;
5; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                    32
                                                                                      2,4-CYCLODIPHOSPHATE SYNTHASE MECPS
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GENERAL INFORMATION:

APPLICANT: Louie, Gordon V.

APPLICANT: Buchanan, Sean Grant

APPLICANT: Bajiwala, Ketan S.

APPLICANT: Sauder, J. Michael

FITTLE OF INVENTION: CRYSTALS AND STRUCTURES OF

TITLE OF INVENTION: 2C-METHLY-D-ERYTHRITOL, 2,4-

FILE REFERENCE: 524982000300

CURRENT APPLICATION NUMBER: US/10/174,410

CURRENT FILING DATE: 2002-06-17

PRIOR APPLICATION NUMBER: 60/299,058

BRIOR FILING DATE: 2001-06-18
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US-10-174-410-136
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US-10-174-410-134
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                                                                                                                                                                                                                                                                    Sequence 136, Applica
Publication No. US200,
GENERAL INFORMATION:
APPLICANT: Louie, Go
APPLICANT: Buchanan
APPLICANT: Sauder,
APPLICANT: Sauder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-174-410-134
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                                   CURRENT APPLICATION NUMBER: US/10/174,410
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 60/299,058
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
SUPPLICATION NOS: 336
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 136
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 336
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 133
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                   APPLICANT: Buchanan, Sean Grant
APPLICANT: Gajiwala, Ketan S.
APPLICANT: Sauder, J. Michael
TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF
TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF
TITLE OF INVENTION: 2C-METHLY-D-ERYTHRITOL, 2,4-CYCLODIPHOSPHATE SYNTHASE MECPS
FILE REFERENCE: 524982000300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: S. typhimurium
ORGANISM: Escherichia coli
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27; Conservative
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1 Similarity 84.48;
27; Conservation
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                                                                                                                                                                                                                                                                                                                 Gordon V.
nan, Sean Grant
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Pred. No. 3.2e-08;
1; Mismatches 4; Indels
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Pred. No. 3.2e-08;
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; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 149; LENGTH: 32; TYPE: PRT; ORGANISM: Escherichia coli US-10-174-410-149
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Search completed: January 29, 2004, 16:21:17 Job time: 10.7171 secs
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US-10-174-410-149
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Best Local S
Matches 27
                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 149, Application US/10174410 Publication No. US20030073134A1 GENERAL INFORMATION:
                                                                                                                                                                         Query Match
Best Local Similarity 84.4%;
                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 524982000300
CURRENT APPLICATION NUMBER: US/10/174,410
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 60/299,058
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Louie, Gordon V.
APPLICANT: Buchanan, Sean Grant
APPLICANT: Gajiwala, Ketan S.
APPLICANT: Gajiwala, Ketan S.
APPLICANT: Sauder, J. Michael
TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF
TITLE OF INVENTION: 2C-METHLY-D-ERVITHRIFOL, 2,
                                                                                                 40 VVLHALADAILGAAALGDIGKHFPDTDPNFKG 71
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                                                                                                                                                        Score 138; DB 15;
Pred. No. 3.2e-08;
1; Mismatches 4;
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Result No. Minimum Maximum Post-processing: Minimum Match Maximum Match Listing first Database Total number of hits satisfying chosen parameters: Title: Perfect score: Scoring table: Sequence: OM protein - protein search, using sw model Searched: 92. Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 80 seq length: 0 seq length: 2000000000 Match January 29, 2004, 15:44:49; Search time 4.61946 Seconds (without alignments) 3268.453 Million cell updates/sec PIR_76:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* Query 283308 segs, 96168682 residues Gapop 10.0 , BLOSUM62 US-09-941-947A-14 MIRVGMGYDVHRFNDGDHII.. Copyright Length GenCore version (c) 1993 - 2004 멾 Gapext 0. 1 0% 1 100% 45 summaries D82311 AB0408 LISSO83 AR85924 AD0858 AR85924 AD08563 AR85924 B91078 AR85924 B91078 AR8701 AR8 A83194 SUMMARIES 5.1.6 Compugen Ltd. .LGFEGRKEGIAVQAVVLIER 157 hypothetical prote hypothetical prote 2-C-methyl-D-eryth conserved hypothet hypothetical prote conserved hypothet conserved hypothet B. subtilis YacN p B. subtilis YacN p hypothetical prote gltX 5'-region con hypothetical prote ygbB/yacN family p conserved hypothet 2C-methyl-D-erythr 2C-methyl-D-erythr 2C-methyl-D-erythr unknown protein, 3 ispd/ispf bifuncti ISPD/ISPF bifuncti hypothetical prote hypothetical prote 2-C-methyl-D-eryth hypothetical 2C-methyl-D-erythr 2C-methyl-D-erythr conserved hypothet Description prote

ALIGNMENTS

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2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase C;Species: Escherichia coli C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #t C;Accession: I55083; F65055 R;Li, C.; Ichikawa, J.K.; Ravetto, J.J.; Kuo, H.C.; FJ. Bacteriol. 176, 6015-6022, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Recession: AB0408
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-162 < KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92590.1; PID:g15981287; GSPDB:GN00C;Gene: 1spF
C;Superfamily: 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.E deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [imported] - Yersinia pestis C;Species: Yersinia pestis C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Dec-2002 C;Accession: AB0408
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C; Superfamily:
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A;Residues: 1-158 <HEI>
A;Cross-references: GB:AE004139;
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Best Local S
Matches 107
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Best Local Similarity
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                                                                                                                                                                                                                DLQCHMDDINVKATTTEQLGFTGRGEGIACEAVVLL
                                                                                                                                                                                                                                                                                                KLFPDTDPAFKGADSRGLLRBAYRRILAKGYKLGNLDITIIAQAPKMAPHIPQMRVNLAE
                                                                                                                                                                                                                                                                                                                                      KHFPDTDPNFKGADSRVLLRHVYGIVKEKGYKLVNADVTIIAQAPKWLPHVPGWRANIAA 119
                                                                                                                                                                                                                                                                                                                                                                                MRIGHGFDVHKFGENGSGPLIIGGVRIPYEKGLLAHSDGDVALHAATDALLGAAALGDIG
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2C-methyl-D-erythritol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.2%; Score 542; DB 68.6%; Pred. No. 5.9e tive 17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN:CAC92590.1; PID:g15981287; GSPDB:GN00175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 554; DB 2;
Pred. No. 4.5e-44;
6; Mismatches 30
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                        Kuo, H.C.; Pu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.9e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
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                                                                #text_change 09-Dec-2002
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                                                                                                          (similarity) -
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                        J.C.; Clarke,
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A;Gene:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-159 <RES>
A;Cross-references: GB:L07942; NID:g1036737; PIDN:AAA79837.1; ER;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; ER;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; EX; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Bscherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F65055
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                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE005174; NID:g12517200; PIDN:AAG57853.1; GSPDB:GN00145; UWGP:Z4(A,Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-159 <STO>
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A;Accession: A85924
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C;Superfamily: 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
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A;Residues: 1-159 <BLAT>
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Best Local S
Matches 107
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  PPDTDPAFKGADSRELLREAWRRIQAKGYTLGNVDVTIIAQAPKKLPHIPQKRVFIAEDL
                            FPDTDPNFKGADSRVLLRHVYGIVKEKGYKLVNADVTIIAQAPKKLPHVPGKRANIAADL 121
                                                                                                                                            IRVGMGYDVHRFNDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGKH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FPDTDPAFKGADSRELLREAWRRIQAKGYTLGNVDVTIIAQAPKMLPHIPQMRVFIAEDL
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                                                                                                                                                                                                                  66.6%; Score 537; DB 2; Length 159; 69.5%; Pred. No. 1.7e-42;
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Burland, V.; Riley, M.;
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DNA Res. 8, 11-22, 2001
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C;Superf
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A; Residues: 1-159 < HAY>
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Reference number: ABD502; MUID:21534947; PMID:11677608
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                                                                                                                                                                                           A; Gene: ECs3600
                                                                                                                                                                                                                            A;Cross-references: GB:BA000007; PIDN:BAB37023.1; PID:gl3363071; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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Residues: 1-159 <PAR>
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                               IRV@MGYDVHRFNDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGKH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCHMDDVNVKATTIEKLGFTGRGEGIACEAVALL 154
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                                                                                                                                                                                                                                                                                                                                                                                                                            Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama,
Kasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
                                                                                                                                                                  2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
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Conservative 14;
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Cronin, A.; Davis, P.; Davi
                                                                                                   69.5%;
                                                                                 Score 537; DB 2;
Pred. No. 1.7e-42;
4; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 537; DB 2;
Pred. No. 1.7e-42;
4; Mismatches 33
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Davies, R.M.; Dowd,
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gltX 5'-region conserved hypothetical protein yacN - Bacillus C;Species: Bacillus subtilis
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A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: F64156
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A; Residues: 1-158 < TIGR>
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C;Accession: F64156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 66.3%; Score 534; DB 2; Similarity 65.6%; Pred. No. 3.2e-42;
                                                                                                                                                                                                                                                                                                                     HEPDTDPNEKGADSRVILLRHVYGIVKEKGYKLVNADVTI IAQAPKMLPHVPGMRANIAAD
                                                                                                                                                                                                            LETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLIER
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                                                                                                                                                               LOCDIEQVNVKATTTEKLGFTGRQEGIACEAVALLIR
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C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #Bequence revision 05-Dec-1997 #text_change 09-Dec-2002
C;Accession: F69741; S66120; ĀS5402
C;Accession: F69741; S66120; ĀS5402
C;Ricust, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterc C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi A.; Eirlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A.; Ehrlich, S.D.; Fintz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc Rayanthors: Poulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc Rayanthors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A., Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Odiega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, R.; Park, S.; Killier, P.; Sato, T.; Scanlon, A.; Aruthors: Schletch, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A.Fitle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A. Accession: F65741
B. Steries mucleic and Sequence of the Gram-positive bacterium Bacillus subtilis. A; Molecule type: DNA A; Residues: 1-158 < KUN; A;Status: nucleic acid sequence not shown; translation not shown

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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A38550; MUID:20512582; PMID:11058132
A;Recession: DB3663
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C;Accession: D83663
C;Accession: Nakas
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A;Accession: A53402
A;Molecule type: DNA
A;Residues: 137-158 <GAG>
A;Cross-references: GB:L14580
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein BH0108 [imported] - Bacillus halodurans (strain C-125)
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A;Residues: 1-158 <CGA>
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C;Superfamily: 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
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A;Noce: the nucleotide sequence was submitted to the EMBL Data Library, December R;Gagdnon, Y; Breton, R.; Putzer, H.; Pelchat, M.; Grunberg-Manago, M.; Lapointe, J._Biol. Chem. 269, 7473-7482, 1994
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A;Experimental source: strain 168
R;Ogasawara, N.; Nakai, S.; Yoshikawa, H.
DNA Res. 1, 1-14, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Clustering and co-transcription of the Bacillus subtilis genes encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Bacillus halodurans
                                                                                                                                                                                                                                                 Superfamily:
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Best Local :
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                                                                                                                                                                                     Similarity
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                                HFPDTDPNFKGADSRVLLRHVYGIVXEKGYKLVNADVTIIAQAFKMLFHVPGMRANIAAD 120
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                                                                                                               MIRVGMGYDVHRFNDGDHIILGGVXIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGK 60
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    HFPDTDPHFKDADSAKLLSAVWELVKEKGYTLGNVDCTIIAQKPKMAPHIPAMRARIAEL
                                                                                 MIRVGQGFDVHQFAEGRILIIGGVEIPYEKGLLGHSDADVLLHTIADAALGAIGEGDIGK
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                                                                                                                                                                                     64.5%; Score 520; 66.5%; Pred. No. 6
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hypothetical protein 1 - Haemophilus ducreyi
C;Species: Haemophilus ducreyi
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Dec-2002
C;Accession: S70845
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A;Molecule type: DNA
A;Residues: 1-160 <TET'>
A;Cross-references: GB:AE002501; GB:AE002098; NID:g7226755; PIDN:AAF41868.1; PID:g722675
                                                                                                                                                                                                        A;Note: the nucleotide sequence was summitted to the problem of a synthase C;Superfamily: 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
                                                                                                                                                                                                                                                                                                A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-160 <PAL>
                                                                                                                                                                                                                                                                                                                                                                                                          R;Palmer, K.L.; Munson Jr., R.S.
Mol. Microbiol. 18, 821-830, 1995
A;Title: Cloning and characterization of the genes encoding the haemolysin of Haemophilu
A;Reference number: S70843; MUID:96422469; PMID:8825086
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A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R. A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58
                                                                                                                                                                                                                                           A;Cross-references: EMBL:U32175; NID:g1151070; PIDN:AAC43539.1; PID:g1151073
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Gene: NMB1512
C,Superfamily: 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
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C;Accession: G81073
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.B.
                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S70845
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                                                                                                             Matches
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                                                                                                                                    Similarity
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MIRIGHGFDVHAFGEKRPLIIGGVTIPYHTGFIAHSDGDVALHALTDALLGAAALGDIGK
                                                     MIRVGMGYDVHRENDGDHIILGGVKIPYBKGLBAHSDGDVVLHALADAILGAAALGDIGK 60
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                                                                                                       62.4%; Score 503; DB 2;
63.1%; Pred. No. 2.4e-39;
tive 17; Mismatches 41
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Pred. No. 1.5e-39;
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HFPDTDPN9KGADSRVLLRHVYGIVKBKGYKLVNADVTIIAQAPKMLPHVPGMRANIAAD

120

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A;Cross-references: GB:AE003962; GB:AE003849; NID:g9106270; PIDN:AAF84103.1; GSPDB:GN001 A;Experimental source: strain 9a5c R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A ae-Neto, B.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H ae-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, W.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigz Chado, M.A.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miraccca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Sa, R.G.; Santelli, R.V.; Sawasak
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C; Date: 05-Ma
C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein XF1294 [imported] - Xylella fastidiosa (strain C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #secuence_revision 20-Aug-2000 #text_change 09-Dec-2002 C;Accession: A82701
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C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                        A; Title: The genome sequence of the plant pathogen Xylella fastidiosa A; Reference number: A82515; MUID:20365717; PMID:10910347 A; Note: for a complete list of authors see reference number A59328 be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: C81867
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                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-176 < SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                        R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer Nature 406, 151-157, 2000
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Pred. No. 2.4e-39;
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    Neisseria meningitidis (strain

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A; Residues: 1-157 < GLA>
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C; Superfamily:
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C;Species: Listeria monocycogeneral C;Species: Listeria monocycogeneral C;Pate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_cost.
C;Accession: AEI104
C;Accession: AEI104
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; R;Glaser, P.; Frangeul, L.; Buchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; 1
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A;Reference number: A59328
A;Contents: annotation
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 294, 849-852, 2001

A; Kuthors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, B.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AB1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:NC_003210; PIDN:CAD00763.1; PID:g16409601; GSPDB:GN00177
A;Experimental source: strain EGD-e
                                                              121 LETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLIER 157
                                                                                                                                         61 FFPDTDMVFKDADSAELLAEIWQKVBADGFRLGNLDATIIAEKPKMAPYVEQMKLRIAEL 120
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31; Mismatches 41; Indels
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. 4.3

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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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806
1 MIRVGMGYDVHRFNDGDHII.....LGFEGRKEGIAVQAVVLIER 157
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        127863 segs, 47026705 residues
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P57708 pseudomonas Q3kuj1 vibrio vuln Q8dc59 vibrio vuln Q871q3 vibrio para Q8zbp7 yersinia pe Q8fej6 escherichia pa 23663 escherichia pa 26673 escherichia pa 26775 bacillus su P44815 haemophilus p57954 pasteurella Q9kgf7 bacillus ha Q8xi08 clostridium Q8xi08 clostridium Q8xi08 clostridium Q8xi08 clostridium Q9kg67 xanthomonas Q8plr7 xanthomonas Q8pdf5 xylella fas Q8pad4 listeria mo Q8r567 fusobacteri Q9ff3 listeria mo Q8r78 thermoanaer Q9ff3 listeria mo Q8r78 thermoanaer Q9ff3 listeria pi pod/ispf Q971x0 clostridium Q92q90 r ispd/ispf Q971x0 clostridipf Q9744 buchnera ap Q94qf0 anabaena sp
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Q9wz.	083525	Q9rn	Q8d2	0256	Q9zm	Q8uf	Q9ca	Q9m4w3	P734	Q9pm	Q8k9d7
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ALIGNMENTS

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RESULT REPORT OF THE SECOND RESULTS OF THE S
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SPF_VIECH

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STANDARD;

PRT; 158 AA.

C Q9KULI;

JT 16-OCT-2001 (Rel. 40, Created)

JT 16-DCT-2001 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE 2-C-methyl-D-erythritol 2,4-cyclodiphosphate syr

"YPTDR) (MECDP-synthase).
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       PROSITE; Pour Prosite; Isoprene )
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                                                                                                 HAMAP; MP 00107; -; 1.
InterPro; IPR003526; YgbB.
Pfam; PF02542; YgbB; 1.
TIGRPAMS; TIGR00151; ispF; 1.
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TIGR;
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STRAIN-E1 Tor N16961 / Serotype 01;
MEDLINE-20406833; PubMed-10952301;
                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (Secons send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 406:477-483(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fifth step SIMILARITY: BELONGS TO THE ISPF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: CONVERTS 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL 2-PHOSPHATE INTO 2C-METHYL-D-ERYTHRITOL 2,4-CYCLODIPHOSPHATE AND CMP. ALSO CONVERTS 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL INTO 2C-METHYL-D-ERYTHRITOL 3,4-CYCLOPHOSPHATE AND CMP (BY SIMILARITY) 2C-METHYL-D-ERYTHRITOL 3,4-CYCLOPHOSPHATE AND CMP (BY SIMILARITY) CATALYTIC ACTIVITY: 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol 2,4-cyclodiphosphatmethyl-D-erythritol 2,4-
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158 AA; 16837 MW;
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Best Local S
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                                            Query Match
                                                                                                Isoprene
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Converts 4-diphosphocytidyl-2C-methyl-D-erythritol 2-
-phosphate into 2C-methyl-D-erythritol 2,4-cyclodiphosphate and
CMP. Also converts 4-diphosphocytidyl-2C-methyl-D-erythritol into
2C-methyl-D-erythritol 3,4-cyclophosphate and CMP (By similarity).
-!- CATALYTIC ACTIVITY: 2-phospho-4-(cytidine 5'-diphospho)-2-C-
methyl-D-erythritol = 2-C-methyl-D-erythritol 2,4-cyclodiphosphate
                                                                                                                                                                                     EMBL; AB016802; AA010006.1; -.
HAMAP MF 001107; -; 1.
InterPro; IPR003526; YgbB.
Pfam; PF02542; YgbB; 1.
                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
2-C-methyl-D-erythritol 2,4-cyclodiphosphate
                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhee J.H., Kim S.Y.,
Choy H.E.;
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Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vibrio vulnificus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is producen the Swiss Institute of Bioinformatics
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biosynthesis; Lyase;
158 AA; 17084 MW;
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                                              Score 551;
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KEDLINB=22508454; PubMed=12620739;

Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Ta
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,

"Genome sequence of Vibrio parahaemolyticus: a pathogenic
distinct from that of V. cholerae.";

Lancet 361:743-749(2003)
                                                                                                                                                                                                                                             EMBL; AP005081; BAC60821.1; --.
HANAP; MF 00107; --; 1.
PROSITE; PS01350; ISPF; 1.
Isoprene biosynthesis; Lyase; (
SEQUENCE 158 AA; 16949 MW;
                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the EM burgean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
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15-SEP-2003 (Rel. 42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L5-SEP-2003
                                                                                                                                                                                                                                                                                                                                              send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Converts 4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate into 2C-methyl-D-erythritol 2,4-cyclodiphosphate and CMP. Also converts 4-diphosphosycidyl-2C-methyl-D-erythritol into 2C-methyl-D-erythritol 3,4-cyclophosphate and CMP (By similarity). CATALYTIC ACTIVITY: 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = 2-C-methyl-D-erythritol 2,4-cyclodiphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fifth step SIMILARITY: BELONGS TO THE ISPF FAMILY.
121
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                                                                                                                        4
                                                                                                                                                                                                     Similarity
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                                                                            HPPDTDPNFKGADSRVLLRHVYGIVKEKGYKLVNADVTIIAQAPKMLPHVPGMRANIAAD
                                                                                                                      MIRIGHGFDVHKFGGEGPVIIGGVAIPYEQGLIAHSDGDVALHALTDALLGAIAAGDIGR
                            LETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLI
                                                            HEPOTODKWKGANSRELLKDVYRRVKEQGYRLGNADVTIMAQAPKWAPHIDAMCAALAED
                                                                                                                                                      MIRVGMGYDVHRENDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HFPDTDPNFKGADSRVLLKHVYGIVKEKGYKLVNADVTIIAQAPKMLPHVPGMRANIAAD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LETDIRNINVKATTTERLGFTGRKEGIATEAVVLL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HFPDTDDKWKGVDSRELLKDVYRRVKEQGYKLGNADVTIIAQAPKMAPYIDAMREAIAHD 120
                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                  69.0%;
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2,4-cyclodiphosphate
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                                                                                                                                                                                    Score 550; DB
Pred. No. 1.8e
19; Mismatches
                                                                                                                                                                                                                                                Complete proteome. F8C9FFA4E03D3D1D CRC64;
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{See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                1.8e-44;
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                                                                                                                                                                                                                  DB 1;
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                                                                                                                                                                                                                 Length 158;
                                                                                                                                                                                    Indels
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RESULT
   Query Match
Best Local S
Matches 107
                                                                     EMBL; AE013685; AAM84414.1; ALT_INIT.
PIR; AB0408; AB0408.
HAMAP; MF_00107; -; 1.
InterPro; IPR003526; YgbB.
Pfam; PF02542; YgbB; 1.
TIGRPAMS; TIGR00151; ispF; 1.
PROSITE; PS01350; ISPF; 1.
Lyase; Isoprene biosynthesis; Complete SEQUENCE 162 AA; 17182 MW; 9A295411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.B., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattn Perry R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEZBP7;
28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21470413; PubMed-11583360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Teltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Telther T., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Leather S., Moule S., Oyston P.C.F., Quail M., Barrell B.G.;

"Genome sequence of Versinia pestis, the causative agent of plague.";

"Genome sequence of Versinia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                        mcdified and this statement
                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of Yersinia pestis KIM.";

Bacteriol. 184:4601-4611(2002).

-!-FUNCTION: Converts 4-diphosphocytidyl-2C-methyl-D-erythritol phosphate into 2C-methyl-D-erythritol 2,4-cyclodiphosphate ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=KIM5 / Biovar Mediaevalis; MEDLINE=22137863; PubMed=12142430;
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                                                                                                                                                                                                                                 EMBL; AJ414156; CAC92590.1; -
                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                       entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CO-92 / Biovar Orientalis; MEDLINE=21470413; PubMed=11586360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
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28-FEB-2003 (Rel. 41, La
28-FEB-2003 (Rel. 41, La
28-C-methyl-D-erythritol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yersinia pestis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISPF OR YPO3360 OR Y0829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphate into 2C-methyl-D-erythritol 2,4-cyclodiphosphate and CMP. Also converts 4-diphosphocytidyl-2C-methyl-D-erythritol into 2C-methyl-D-erythritol 3,4-cyclophosphate and CMP (By similarity). 2C-methyl-D-erythritol 3,4-cyclophosphate and CMP (By cimilarity). CATALYTIC ACTIVITY: 2-phospho-4 (cytidine 5'-diphospho)-2-C-methyl-D-erythritol 2,4-cyclodiphosphate
                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fifth step SIMILARITY: BELONGS TO THE ISPF FAMILY.
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IM5 / Biovar Mediaevalis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yersinia.
                    67.2%;
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Last annotation update)
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Score 542; DB
Pred. No. 1e-4:
17; Mismatches
                                                                         Complete proteome 9A295411D3DFB1EB
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                    542; DB 1
No. 1e-43;
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                                                                                                                                                                                                                                                                                                                                                          is produced through a collaboration -
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                                     DB 1;
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107;

Conservative

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Indels

2

Gaps

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Similarity

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XX MEDLINE-2238934; PubMed=12471157;
XA MEDLINE-2238934; PubMed=12471157;
XA Melch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
XA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
XA Mayhew G.F., Rose D.J., Zhou S., Schwattz D.C., Perna N.T.,
XA Mobley H.L.T., Donnenberg M.S., Slattner F.R.;
YET "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002),
Proc. Natl. Acad. Sci. U.S.A. 39:17020-17024(2002),
Proc. Natl. 
                                                                                                                                                                     Query Match
Best Local
                                                                                                                                           Matches
                                                                                                                                                                                                                               TIGRFAMS; TIGRO0151; ispF; 1.

PROSITE; PS01350; ISPF; 1.

Isoprene biosynthesis; Lyase; Complete proteome.

SEQUENCE 159 AA; 16867 MW; 8FD4573623BA4549 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as accept Usage by and for commercent modified and this statement is not removed. Usage by and for commercent modified and this statement is not removed. Usage by and for commercent modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli 06
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15-SEP-2003 (Rel. 42, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8FEJ6;
15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=217992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISPF OR C3313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (EC 4.6.1.12) (MECDP-synthase).
                                                                                                                                                                                                                                                                                                              InterPro; Irave-
ofam; PF02542; YgbB;
                                                                                                                                                                                                                                                                                                                                                                                     HAMAP;
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE016765; AAN81762.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: Nonmevalona SIMILARITY: BELONGS
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                                                                                                                                           107;
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ro; IPR003526; YgbB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KHEPDTIDENEKGADSRVLLRHVYGIVKEKGYKLVNADVTIIAQAPKMLPHVEGMRANIAA
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FPDTDPNFKGADSRVLLRHVYGIVKEKGYKLVMADVTIIAQAPKMLPHVPGMRANIAADL
                                                                              IRVGMGYDVHRFNDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGKH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLFPDTDPAFKGADSRGLLREAYRRILAKGYKLGNLDITIIAQAPKMAPHIPQMRVNLAE 120
                                           MRICHGFDVHAFGGEGPIIIGGVRIPYEKGLLAHSDGDVALHALTDALLGAAALGDIGKL
                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nonmevalonate terpenoid biosynthesis pathway; TY: BELONGS TO THE ISPF FAMILY.
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                                                                                                                                         14;
                                                                                                                                         Score 537; DB 1
Pred. No. 3e-43;
4; Mismatches
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RESULT 7
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MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck S.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Wature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=E.coli; STRAIN=K12 / MG1655;
KEDLINE=97426617; PubMede-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose [
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Studies on the nonmevalonate pathway: formation of 2-C-me erythritol 2,4-cyclodiphosphate from 2-phospho-4-{cytidine diphospho}-2-C-methyl-D-erythritol.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2C-methyl-D-erythritol cyclodiphosphate.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li C., Ichikawa J.K., Ravetto J.J., Kuo H.-C., Fu J.C., Clarke
"A new gene involved in stationary-phase survival located at 50
minutes on the Escherichia coli chromosome.";
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MEDLINE=95014035; PubMed=7928962;
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NCBI_TaxID=562, 83334, 623;
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Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=E.coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biosynthesis of terpenoids: YgbB
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OR MECS OR B2746 OR Z4054 OR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wungsintaweekul J., Schuhr C., Fellermeier M., Eisenreich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCHMDDVNVKATTTEKLGFTGRGEGIACEAVALL 154
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29, Last seq
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                                                                                                                                                                                                                                                                                                                                                         Escherichia coli K-12. *;
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e to 2C-methyl-D-erythritol 2,4-
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formation of 2-C-methyl-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ጅ
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Zenk M.H.,
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PDB; 13X1; 16 MAY-02.

PDB; 13Y6; 30-JAN-02.

PDB; 1XW; 18-JUN-02.

PDB; 1KNX; 18-JUN-02.

ECGene; EG11816; ispF.

HAMAP; MF 00107; -; 1.

InterPro; IPR003526; YgbB.

Pfam; PF02542; YgbB; 1.

Pfam; PF02542; YgbB; 1.

PROSITE; PS01350; ISPF; 1.

Lysse; Isoprene biosynthesis; Magnesium; Manganese; Com
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SPECIES-S.flexneri; STRAIN-301 / Serotype 2a;
MEDLINE-22272406; PubMed-12384590;
Uin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Ou D., Dong J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Yang J., Yang F., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Wen Y., Hou Y.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                between the wass investigated. There are no testime the European Bioinformattics Institute. There are no testime in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogaswara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterchemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Electrophoresis 20:2181-2195(1999).

-!- FUNCTION: CONVERTS 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL 2-PHOSPHATE INTO 2C-METHYL-D-ERYTHRITOL 2, 4-CYCLODIPHOSPHATE AND CMP. ALSO CONVERTS 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL INTO 2C-METHYL-D-ERYTHRITOL 3, 4-CYCLOPHOSPHATE AND CMP.

-!- CATALYTIC ACTIVITY: 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = 2-C-methyl-D-erythritol 2, 4-cyclodiphosphate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fountoulakis M., Takacs M.-F., Berndt P., Langen H., "Enrichment of low abundance proteins of Escherichia hydroxyapatite chromatography.";
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
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; H91078; H91078.
; I55083; I55083.
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PATHWAY: Nonmevalonate terpenoid biosynthesis
SIMILARITY: BELONGS TO THE ISPF FAMILY.
                                                                                                                                                                                                                                                                         ; U29579; AAA69256.1;
; AE0000358; AAC75788.1; -..;
; AE005502; AAG57853.1; -..;
; AE005262; BAB37023.1; -..;
; AE015291; AAN44258.1; -..;
                                                                                                                                                                                                                                                                                                                                                                   AF230738; AAF44656.1; -. AB038256; BAA95145.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                              AAA79837
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             Complete proteome;
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                                                                                                                      This SWI
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Eaker S., Basham D., Brooks K., Chillingworth T., Connerton P., Eaker S., Davis P., Davies R.M., Dowd L., White N., Farrar J., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
                                                                                                                                                                                                                                                                                    J. Bacteriol. 185:2330-2337(2003).

-!- FUNCTION: Converts 4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate into 2C-methyl-D-erythritol 2,4-cyclodiphosphate and CMP. Also converts 4-diphosphocytidyl-2C-methyl-D-erythritol into 2C-methyl-D-erythritol 3,4-cyclophosphate and CMP (By similarity).

-!- CATALYTIC ACTIVITY: 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = 2-C-methyl-D-erythritol 2,4-cyclodiphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISPF SALTI
Q8Z472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRALN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plumkett G. III, Mayhew G.F.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner
"Comparative genomics of Salmonella enterica serova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
2-C-methyl-D-crythritol 2,4-cyclodiphosphate synthase (EC 4.6.1.12)
(MECPS) (MECDP-synthase).
ISPF OR STY3054 OR T2830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
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                                                    ween the Swiss Institute of Bioinf European Bioinformatics Institute by non-profit institute.
                                                                                                                                                                                                   PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fifth step SIMILARITY: BELONGS TO THE ISPF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CT18.";
                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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107; Conserv
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69.5%; Pred. No. 3e--
tive 14; Mismatches
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RESULT REPLET ON SOLUTION OF THE SECOND STATES OF T
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EMBL; AZ016843; AAO70387.1; -.
HAMAP; MF 00107; -; 1.
InterPro; IPR003526; YgbB,
Pfam; PF02542; YgbB; 1.
TIGREAMS; TIGR00151; ispF; 1.
PROSITE; PS01350; ISPF; 1.
Lysse; Isoprene biosynthesis; COSEQUENCE 159 AA; 16885 MW; 1
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Q8ZMF7;
                        This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
2-C-methyl-D-erythritol 2,4-cyclodiphosphate (MECPS) (MECPsynthase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 413:852-856(2001).
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STRAIN=LT2 / SGSC1412 / AFCC 700720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of Salmonella enterica
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                                                                                                                                                                                                                                                        PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fifth step SIMILARITY: BELONGS TO THE ISPF FAMILY.
                                                                                                                                                                                                                                                                                                                                         FUNCTION: Converts 4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate into 2C-methyl-D-erythritol 2;4-cyclodiphosphate and CMP. Also converts 4-diphosphocytidyl-2C-methyl-D-erythritol into 2C-methyl-D-erythritol 3,4-cyclophosphate and CMP (By similarity). CATALYTIC ACTIVITY: 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = 2-C-methyl-D-erythritol 2,4-cyclodiphosphate
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Pred. No. 3e-43
14; Mismatches
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5 outstation -
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PRESENTATION OF THE PRESEN
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Best Local Sim
Matches 107;
MEDINE-9044033; PubMed-9384377;
MEDINE-90404033; PubMed-9384377;
MEDINE-9040 V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Ravedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton IF., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Entian K.D., Errington J., Fabret C., Ferrari B., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galileron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  StyGene; SG?????; ispF.
HAMAP; MF_00107; -; 1.
InterPro; IPR003526; YgbB.
Pfam; PF02542; YgbB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=94171772; Gagnon Y., Breton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
2-C-methyl-D-erythritol 2,4-cyclodiphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206756;
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PROSITE; PS01350; ISFF; 1.

Lyase; Isopprene biosynthesis; Complete proteome.

SEQUENCE 159 AA; 16899 MW; 9FD88D2C95662939 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ogasawara N., Nakai S., Yoshikawa
"Systematic sequencing of the 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Clustering and co-transcription of the Bacillus subtilis genes encoding the aminoacyl-tRNA synthetases specific for glutamate or cysteine and the first enzyme for cysteine biosynthesis.";
J. Biol. Chem. 269:7473-7482(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE008833; AAL21809.1;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96051385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MECPS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              cnromosome containing i:1-14(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPDTDPAFKGADSRELLREAWRRIQAKGYTIGNVDVTIIAQAPKKLPHIPQKRVFIAEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FPDTDPNFKGADSRVLLRHVYGIVKEKGYKLVNADVTIIAQAPKMLPHVPGMRANIAADL
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R., Putzer H., Pelchat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.5%;
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Pred. No. 3e-43;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
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kilobase region of the
e replication origin.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EC 4.6.1.12)
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RESULT
ISPF HA
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DT 01
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Best Local S
Matches 103
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RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Presecan E., Pujic P., Purnelle D., Rapport G., Rey M., Reynolds S.,

Raieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

Sorokin A., Tacconi E., Takaji T., Takahashi H., Takemaru K.,

RA Sekiguchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Vassarotti A.,

RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,

RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,

Winters P., Wipat A., Yanamoto H., Yamane K., Yasumoto K., Yata K.,

"The complete genome sequence of the Gram-positive bacterium Bacillus authilis ""
ISPF HAEIN
P44815;
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF02542; YgbB; 1.
TIGRFAMs; TIGR00151; ispF; 1.
PR0SITE; PS01350; ISPF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; F69741; F69741.
SubtiList; BG10153; ispF.
HAMAP; MF_00107; ; 1
InterPro; IPR003526; YgbB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is content (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: CONVERTS 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL 2-PHOSPHATE INTO 2C-METHYL-D-ERYTHRITOL 2,4-CYCLODIPHOSPHATE AND CMP. ALSO CONVERTS 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL INTO 2C-METHYL-D-ERYTHRITOL 3,4-CYCLOPHOSPHATE AND CMP (BY SIMILARITY).

CATALYTIC ACTIVITY: 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol 2,4-cyclodiphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fifth step SIMILARITY: BELONGS TO THE ISPF PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D26185;
Z99104;
                                                                                                                                                                                     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Isoprene biosynthesis; Complete proteome.
CE 158 AA; 17126 MW; ED11D03EC3752BD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                            HEPDTDPNFKGADSRVLLRHVYGIVKEXGYKLVNADVTIIAQAPKMLPHVPGMRANIAAD
                                                                                                                                               LEADVSQVNVKATTTEKLGFTGRAEGIAAQATVLIQK 157
                                                                                                                                                                                   LETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLIER 157
                                                                                                                                                                                                                    HFPDTDPEFKDADSFKLLQHVWGIVKQKGYVLGNIDCTIIAQKPKMLPYIEDMRKRIAEG
                                                                                                                                                                                                                                                                                                 MFRIGQGFDVHQLVBGRPLIIGGIEIFYBKGLLGHSDAD
                                                                                                                                                                                                                                                                                                                 MIRVGMGYDVHRENDGDHIILGGVKIFYEKGLEAHSDGDVVLHALADAILGAAALGDIGK
 (Rel.
                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; AAA21795.1; -.; BAA05325.1; -.; CAB11867.1; -.
                                                       STANDARD;
32,
                                                                                                                                                                                                                                                                                                                                                                                        65.68;
   Last
                     Created)
                                                                                                                                                                                                                                                                                                                                                                          18;
 sequence
                                                                                                                                                                                                                                                                                                                                                                        Score 534; DB
Pred. No. 5.6e
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      DB 1; L
5.6e-43;
les 36;
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 158;
                                                                                                                                                                                                                                                                                               VLLHTVÅDACLGAVGEGDIGK
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Matches
                                                                                                                      Query Match
Best Local
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InterPro; IPR003526; YgbB.
Pfam; PF02542; YgbB; 1.
FIGRPAMs; TIGR00151; ispF; 1.
FROSITE; PS01350; ISFF; 1.
Lyase; ISoprene biosynthesis; C.
SEQUENCE 158 AA; 17194 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib-
                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Electrophoresis 19:1819-1827(1998).

-: FUNCTION: CONVERTS 4-DIPHOSPHACTEDIPL-2C-METHYL-D-ERYTHRITOL 2-PHOSPHATE AND PHOSPHATE AND CONVERTS 4-DIPHOSPHATE TOL 2,4-CYCLODIPHOSPHATE AND CMP. ALSO CONVERTS 4-DIPHOSPHACYTIDYL-2C-METHYL-D-ERYTHRITOL INTO 2C-METHYL-D-ERYTHRITOL 3,4-CYCLOPHOSPHATE AND CMP (BY SINILARITY).

-:- CATALYTIC ACTURITY: 2-phospho-4-(cytidine 5'-diphospho)-2-(c-CATALYTIC ACTURITY).

-:- CATALYTIC ACTURITY: 2-C-methyl-D-erythritol 2,4-cyclodiphosphate
                                                                                                                                                                                                                                                                                         PIR; F64156; F64156.
PDB; 1JN1; 21-AUG-02.
TIGR; HI0671; -.
                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION BY MASS SPECTROMETRY. MEDLINE=98384070; PubMed=9719565; Fountoulakis M., Juranville J.F., Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=RG / NM20 / MEDLINE=95350630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gam
Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-SEP-2003 (Rel. 42, Last annotation update)
2-C-methyl-D-erythritol 2,4-cyclodiphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 269:496-512(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Reference map of the low molecular mass proteins of Haemophilus influenzae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             angen H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPF OR HI0671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fifth step SIMILARITY: BELONGS TO THE ISPP FAMILY.
                                                                                                     103;
                                                                                                                                                                                                                                                                                                                                            U32750; AAC22331.1;
                                  μ
                                                                                                                      Similarity
                                  (MECDP-synthase).
HFPDTDPNFKGADSRVLLRHVYGIVKEKGYKLVNADVTI IAQAPKMLPHVPGMRANIAAD
                                                                                                     Conservative
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                                                                                                   20;
                                                                                                   Score 534; DB 1;
Pred. No. 5.6e-43;
0; Mismatches 34
                                                                                                                                                                     Complete proteome; 3D-structure. DC34BF347DEC2BFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roder D.,
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                                                                                                                                  Length 158;
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LFPDTDMQYKNADSRGLLREAFRQVQEKGYKIGNVDITTIAQAPKMRPHIDAMRAKIAED

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LETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLIER 157

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Best Local :
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P57954;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE006198; AAK03693.1; -.
HAMAB; MF 00107; -; 1.
InterPro; IPR003526; YgbB,
Pfam; PF02542; YgbB; 1.
TIGRFAMs; TIGR00151; ispF; 1.
TROSITE; PS01350; ISPF; 1.
LYASE; Isoprene biosynthesis; Complete proteome.
SEQUENCE 158 AA; 16555 MW; 35B9CBA59147171E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-i- FUNCTION: CONVERTS 4-DIPHOSPHCYTIDYL-2C-METHYL-D-ERYTHRITOL 2-
PHOSPHATE INTO 2C-METHYL-D-ERYTHRITOL 2,4-CYCLODIPHOSPHATE AND
CMP. ALSO CONVERTS 4-DIPHOSPHCYTIDYL-2C-METHYL-D-ERYTHRITOL INTO
2C-METHYL-D-ERYTHRITOL 3,4-CYCLOPHOSPHATE AND
CCMP. ALSO CONVERTS 4-DIPHOSPHCTYIDYL-2C-METHYL-D-ERYTHRITOL 3,7-CYCLOPHOSPHATE AND CMP (BY SIMILARITY).
-i- CATALYTIC ACTIVITY: 2-phospho-4-(cytidine 5'-diphospho)-2-C-
methyl-D-erythritol = 2-C-methyl-D-erythritol 2,4-cyclodiphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
2-C-methyl-D-erythritol 2,4-cyclodiphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fifth step. SIMILARITY: BELONGS TO THE ISPF FAMILY.
   121
                                                                                                                                                                                                                                                                                                                                                                                          105;
                                                                                                                                 61
                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
LACDIEQVNVKATTSERLGFTGRGEGIACEAVALV
                                                             LETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLI 155
                                                                                                                                                                                    HFPDTDENEKGADSRVLLRHVYGI VKBKGYKLVNADVTI IAQAEKMLEHVEGMRANIAAD
                                                                                                                                                                                                                                                        MIRIGHGFÐVHAFGGEGPIIIGGVAIPYEKGLLAHSDGDVALHALTDALLGAVALGDIGK
                                                                                                                                                                                                                                                                                          MIRVGWGYDVHRFNDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGK
                                                                                                                          LFPDTDMQYKGADSRGLLREAYTQVQAKGYKVGNVDVTIIAQAPKMRPHIDAMRAAIAED
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                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              65.6%;
                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                            Score 529; DB
Pred. No. 1.7e
15; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 158; .7e-42; es 35; Indels
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RESULT 13

33335 5

"ISPF NEIMB Q9JYMS; 16-OCT-2001 16-OCT-2001 28-FEB-2003

STANDARD;

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(Rel. 40, Created)
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RESULT 14
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Best Local
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HAMAP; MF 00107; -; 1.

InterPro; IPR003526; YgbB.

Pfam; PF02542; YgbB; 1.

TIGRFAMs; TIGR00151; ispF; 1.

PROSITE; P801350; ISFF; 1.
   NEIMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lyase; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               halodurans and genomic sequence comparison with Bacillus subtilis.";

Nucleic Acids Res. 28:4317-4331 (2000)

-i- FUNCTION: CONVERTS 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL 2-PHOSPHATE INTO 2C-METHYL-D-BRYTHRITOL 2,4-CYCLODIPHOSPHATE AND CYP. ALSO CONVERTS 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL INTO 2C-METHYL-D-ERYTHRITOL 3,4-CYCLOPHOSPHATE AND CYP. (BY SIMILARITY).

-i- CATALYTIC ACTIVITY: 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = 2-C-methyl-D-erythritol 2,4-cyclodiphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9KGF7;
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP001507; BAB03827.1;
PIR; D83663; D83663.
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Takami H., Nakasone K., Takaki Y., Maeno G., Si
Puji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus halodurans.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (BC 4.6.1.12)
(MECPS) (MECDP-synthase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete genome sequence of the alkaliphilic bacterium Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103;
                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isoprene biosynthesis; Complete proteome CB 157 AA; 16751 MW; 0205862C7B69EA99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                       HFPDTDPNFKGADSRVLLRHVYGIVKEKGYKLVNADVTIIAQAFKMLPHVFGMRANIAAD
                                                                                                                                                                                                                                                                                                                                                                              MIRVGMGYDVHRPNDGDHIIIGGGVKIPYBKGLBAHSDGDVVLHALADAILGAAALGDIGK
                                                                                                                                                                       LETOVOFINVKATTTEKLGFEGRKEGIAVQAVVLI 155
                                                                                                                                                                                                                                                                                                                                                     MIRVGQGFDVHQFAEGRLLIIGGVEIPYEKGLLGHSDADVLLHTIADAALGAIGEGDIGK
                                                                                                                  LEARBAQVNVKATTTETLGFTGRGEGIASQAVILL
                                                                                                                                                                                                                                     HFPDTDPHFKDADSAKLLSAVWELVKEKGYTLGNVDCTIIAQKPKMAPHIPAMRARIAEL
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Pred. No. 1.1e-41;
%6; Mismatches 36
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., Kuhara S
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RESULT 15
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Matches 95
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HAMAP, MP.00107; -; 1.

InterPro; IPR003526; YgbB.

Pfam; PF02542; YgbB; 1.

TIGR2AMs; TIGR00151; ispF; 1.

PROSITE; PS01350; ISPF; 1.

Lyase; Isoprene biosynthesis; Complete proteome.

Lyase; Isoprene biosynthesis; Complete proteome.

Lyase; Isoprene biosynthesis; Complete proteome.
                 ISPE_HAEDU
Q47956;
   30-MAY-2000
                                                         HAEDU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tettelin H.; Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Haft D.H., Clark S.B., Cittone H., Clark S.B., Cotton T., Ciecko A., Parksey D.S., Blair B., Cittone H., Clark S.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C., "Complete genome sequence of Neisseria meningitidis serogroup B strain MCC38 n.
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STRAIN=MC58 / Serogroup B;
MEDLINE=20175755; PubMed=10710307;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis (serogroup B).
Bacteria, Proteobacteria; Betaproteobacteria, Neisseriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (BC 4.6.1.12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: CONVERTS 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL 2-PHOSPHATE INTO 2C-METHYL-D-ERYTHRITOL 2,4-CYCLODIPHOSPHATE AND CMP. ALSO CONVERTS 4-DIPHOSPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL 1NTO 2C-METHYL-D-ERYTHRITOL 3,4-CYCLOPHOSPHATE AND CMP (BY SIMILIARITY).

CATALYTIC ACTIVITY: 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = 2-C-methyl-D-erythritol 2,4-cyclodiphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fifth step. SIMILARITY: BELONGS TO THE ISPF FAMILY.
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                                                                                                                                                                     STDVDFINVKATTTEKLGFEGRKEGIAVQAVVLIER 157
                                                                                                                                                                                                                               FPDTDPNFKGADSRVLLRHVYGIYKEKGYKLVMADVTIIAQAPKMLPHVPGMRANIAADL
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 39, Created)
                                                                                                                                                                                                                                                                                                                                                                             62.7%;
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Pred. No. 2.
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2.9e-40;
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-!- FUNCTION: CONVERTS 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL 2-PHOSPHATE INTO 2C-METHYL-D-ERYTHRITOL 2.

--- PHOSPHATE INTO 2C-METHYL-D-ERYTHRITOL 2.

CMP. ALSO CONVERTS 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL INTO 2C-METHYL-D-ERYTHRITOL 3,4-CYCLOPHOSPHATE AND CMP (BY SIMILARITY).

--- CATALYTIC ACTIVITY: 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol 2,4-cyclodiphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Palmer K.P., Munson R.S. Jr.;
"Cloning and characterization of the genes encoding the hemolysin Haemophilus ducreyi.";
                                                                                                                                                                                                                                                                                                     HAMAP; MF_00107; -; 1.
interPro; IPR003526; YgbB.
Pfam; PF02542; YgbB; 1.
TIGRPAMs; TIGR00151; ispF; 1.
PROSITE; PS01350; ISPF; 1.
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28-FEB-2003 (Rel. 41, Last annotation update)
2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (BC 4.6.1.12)
(MECDP-synthase)
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Pasteurellaceae; Haemophi
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S70845; S70845.
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                                                                LFPDTDQQYKNIDSRKLLIEAYRQYQTKGYQISNIDITIIAQAPKWRPHIDNWRQLIAND
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                              LETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLIER
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AA; 17437 MW;
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Pred. No. 4.5e-40;
L7; Mismatches 41
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Title:
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                        Q890h4 brucella su
Q8dh64 synechococc
Q8f0a5 leptospira
Q8d224 wiggleswort
Q8rqp5 thermus the
Q8g512 bifidobacte
Q8fm14 corymebacte
Q8eua4 mycoplasma
Q8kx66 synechococc
                                                                                                        Q8ebr3 shewanella
Q8dc59 vibrio vuln
Q8fej6 escherichia
Q8kc25 chlorobium
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       Q8efr7 shewanella
Q8lbv9 arabidopsis
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ALIGNMENTS

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RESULT 1
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                                                                                                                          Query Match
Best Local Similarity
Matches 111; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-22297686; PubMed-12368813;
Heidelberg J.F., Paulsen I.T., Nelson K.E., Galdos E.J., Nelson W.C., Read T.D., Bisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Neyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., Neyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Lee C., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Vamathevan J., Weidman J., Topraim M., Lee R., McDonald L.A., Praser C.M.; Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
20-methyl-p-erythritol 2,4-cyclodiphosphate synthase.
ISPF OR SO3437.
                                                                                                                                                                                                                                                                                                         Nat. Biotechnol. 20:1118-1123(2002).
EMBL; AE015780; AAN56434.1; .
TIGR; S03437; ..
Complete proteome.
SEQUENCE 159 AA; 16995 MW; A16DC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=MR-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alteromonadaceae; Shewanella.
NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shewanella oneidensis.
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2 IRVGMGYDVHRFNDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGKH
                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                               70.6%; Score 569; DB 16; 71.2%; Pred. No. 2.7e-45; tive 17; Mismatches 28;
                                                                                                                                                                                                                                                                                                                       A16DC82586297501 CRC64;
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                                                                                                                                                                                                                         Length 159;
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RESULT 3
RESULT 02-M
RESULT 01-M
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01-MAR-2003 (TrEMBLrel. 2

01-MAR-2003 (TrEMBLrel. 2

01-MAR-2003 (TrEMBLrel. 2

2-C-methyl-D-erythritol 2

4.6.1.12).
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                                        STRAIN=06:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; Pubmed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Ro
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                           Escherichia coli 06.
Bacteria; Proteobacteria;
Enterobacteriaceae; Eschei
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Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              NCBI_TaxID=217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                      YGBB OR C3313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8FEJ6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vibrio vulnificus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete
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    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 551; DB 16;
Pred. No. 1.3e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OE888FE050160112 CRC64;
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Best Local :
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Q8KC25;
01-OCT-2002
01-OCT-2002
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"The complete genome sequence of Chlorobium tepidum TJS, a photosynthetic, anaerobic, green-sulfur bacterium.";
Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).

EMBL; AB012915; AAM72826.1; -.
                                                                                                                                                                                                                                                                                              Complete
SEQUENCE
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01-OCT-2002 (TrEMBLrel. 22, Last Sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase.
ISSF OR CT1601.
Chlorobium tepidum.
Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobi
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"Extensive mosaic structure revealed by the complete
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
EMBL; AB016765; AAN81762.1;
Lyase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                          Pfam; PF02542; YgbB; 1.
TIGRFAMs; TIGR00151; ispP;
PROSITE; PS01350; ISPF; 1.
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STRAIN=TLS / ATCC 49652 / DSM 12025;
MEDLINE=22103685; PubMed=12093901;
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157 AA;
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                                 FPDTDPNFKGADSRVLLRHVYGIVKEKGYKLVNADVTIIAQAPKMLPHVFGMRANIAADL
                                                                                             ETDVDFINVKATTTEKLGPEGRKEGIAVQAVVLI 155
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FPDTSPDYKDADSMELLRHVCKLLBQEGYKFVNVDTMLLLEKFKIAFYIDQMRRNIARCL
                                                                                                                          IRVGMGYDVHRFNDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGKH
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                                                                                                                                                                                                                                                                                              16923 MW; 4FA5A7DCB20C8B7B
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                                                                                                                                                                                                33;
                                                                                                                                                                                                Score 453; DB
Pred. No. 1.8e
33; Mismatches
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Pred. No. 2.6e-42;
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RESULT 6
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AC Q8DH
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DT 01-
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Matches 79
                                                                                                                                                                                                                                                                                                                                                                                                       QBDHC4;
QBDHC4;
QBDHC4;
QLAMAR-2003 (TERMBLrel. 23, Created)
QLAMAR-2003 (TERMBLrel. 23, Last sequence update)
QLAMAR-2003 (TERMBLrel. 23, Last annotation update)
QLAMAR-2003 (TERMBLrel. 23, Last annotation update)
QLAMAR-2003 (TERMBLrel. 23, Created)
QBDHC4;
QB
MEDLINE=2225144; PubMed=12240834; Meuchi M., Katoh H., Sasamoto Makamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto Watanabe A., Iriquchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
                                                                                                                                                                                                                                                                                                                                                              Synechococcus elongatus (Thermosynechococcus elongatus). Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
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STRAIN=1330 / Biovar 1;
MEDLINE=22247741; PubMed=12271122;
                                                                                                                                                                                     STRAIN-BP-
                                                                                                                                                                                                                                   SEQUENCE
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
2C-methyl-D-erythricol 2,4-cyclodiphosphate
synthase/4-diphosphocytidyl-2C-methyl-D-erythritol synthase.
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                                                                                                                                                                                                                                                                                                                eria; Cyanobacteria;
_TaxID=32046;
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Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
AE014413; AAN30040.1; -.
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                                                                                                                                                                                                                                                                                                                                                     Chroococcales;
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Best Local :
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Complete proteome.

SEQUENCE 161 AA; 17651 MW; 625A49B3223D22C9 CRC64;
   Wigglesworthia
                                                                  YgbB protein.
                                                                                                                                                                                                                                                    Q8D224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Spirochaetes;
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Pred. No. 4.5e-26;
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Pred. No. 5.8e-29;
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Best Local
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OBROPS;
O1-JUN-2002 (TrEMBLrel.
O1-JUN-2002 (TrEMBLrel.
O1-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (1)
SEQUENCE FROM N.A.
MEDLINE=22297718; PubMed=12219091;
MEDLINE=22297718; PubMed=12219091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yokoyama S., Tame J.R., Park S.;
"2-C-methyl-D-erythritol 2,4-cyclodiphosphate
thermophilus HB8.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kishida H., Wada T., Un
Yokoyama S., Tame J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2-C-methyl-D-erythritol (EC 4.6.1.12).
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Nat. Genet. 32:402-407(2002).
EMBL; AB063522; BAC24677.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aksoy
Aksoy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2002) to the EMBL/GenBank/DDBJ EMBL; AB082126; BAB86885.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermus thermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YGBB.
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=HB8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Deinococcus-Thermus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pro; IPR003526; YgbB.
Pr02542; YgbB; 1.
MMs; TIGR00151; ispF; 1.
                                                               62
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                                                                                                                                                             IRVGMGYDVHRENDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGKH
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                                                                                                                               MRIGYGEDSHRI
FPDTDPRWRGERSEVFLREALRLVEARGAKLLQASLVLTLDRPKLGPHRKALVDSLSRLL
                                                         FPDTDPNFKGADSRVLLRHVYGIVKEKGYKLVNADVTIIAQAPKMLPHVPGMRANIAADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IKCKTOVINIKSKTMEGIGEIGKKKGIASEAVSVILE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LETDVDFINVKATTTEKLGFEGRKEGIAVQAV-VLIB 156
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                                                                                                                                                                                                                                                                                                                                                                                152 AA;
                                                                                                                                                                                                                                                 33.7%;
ilarity 39.4%;
Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 AA; 17252 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.9%;
llarity 45.2%;
Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                             16520 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Park S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21, Created)
21, Last sequence update)
22, Last annotation update)
22, 4-cyclodiphoshate synthase
                                                                                                                                                                                                                                                 25;
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Pred. No. 5.8e-23;
7; Mismatches 46
                                                                                                                                                                                                                                                 Score 272; DB 2;
Pred. No. 1.3e-17;
5; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                             0114C0E440DC28F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kuzuyama T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deinococci;
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                                                                                                                                                                                                                                                 65;
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                                                                                                                                                                                                                                                                                                       Length 152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shirouzu M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OSEMI4 PRELIMINARY; PRT; 171 AA.

OSEMI4; OSEM
                                                                                                                              SEQUENCE FROM N.A.

STRALN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H.,
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi
Usuda Y., Sugimoto S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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Bacteria; Actinobacteria; Actinobact
Bafidobacteriaceae; Bifidobacterium.
                                             "The entire genomic sequence of Corynebacterium efficiens Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomyce
Corynebacterineae; Corynebacteriaceae; Corynebacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium efficiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conserved hypothetical protein.
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Pessi G., Zwahlen M.-C., I
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    Created)
    Last sequence update)
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Synechococcus sp. (strair Bacteria; Cyanobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE=22354719; PubMed=12466555; Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.; "The complete genomic sequence of Mycoplasma penetrans, intracellular bacterial pathogen in humans."; Nucleic Acids Res. 30.5293-5300(2002).
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01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
01-there enzyme of deoxy-xylulose pathway YgbB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP004174; BAC44812.1; -. Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycoplasma penetrans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=28227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVGMGYDVHRF-NDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGKH 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIETDVD--FINVKATTTEKLGFEGRKEGIAVQAVVLIER 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSDTDSKNKNLDSLEILSMCLNELKKQDYSISNVDITIICE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FPDTDPNFKGADSRVLLRHVYGIVKEKGYKLVNADVTIIAQAPKMLPHV--PGMRANIAA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIGNGIDIHKIKKEKCKQRLAGLDFELDYKIIAHSDGDIILHSISSAILGALSLQDLGTY 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTDPNFKGADSRVILRHVYGIVKBKGYKLVNADVTIIAQAPKMLPHVPGMRANIAADLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 AA; 19038 MW; C6851C7B8FFBC5C4 CRC64;
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                               (strain PCC 7002) (Agmenellum quadruplicatum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.1%;
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      Chroccoccales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 194; DB 16;
Pred. No. 2.7e-10;
6; Mismatches 57
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Pred. No. 1.2
                                                                                                                                                                                                                                                                                                                                                                                                                              -YEEDKUMIQUNTVLLINK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165
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Hattori M.;
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                                                                                                (Fragment).
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QREPR/
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Best Local S
Matches 37
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local 9
                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Bisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Bearnam M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vanathevan J., Weidnam J., Impraim M., Lee K., Berry K., Lee C., Wieller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Miller G., Weidnam J., Weiter J.C., Nealson K.H., Fraser C.M., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis."
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QSEFR7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nomura C.T., Persson S., Zhao J., Bryant D.A.;
"An Analysis of Forty Genes Encoding Electron Transport Proteins from
Synechococus sp. PCC 7002: A Comparative Study of Electron Transport
Proteins from Cyanobacteria and Chloroplasts.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF381048; AAN03587.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nat. Biotechnol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22297686; PubMed=12368813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shewanella oneidensis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SO1899.
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                                  198 YHQLKQYLAHYKDLAARYPFTTIPYTEVIKPGTTSPSIKGIAAR
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                                                                                                                                                                                                                                                                                                                                                                                                                       nl protein; Complete
571 AA; 64713 MW;
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Pred. No. 2.4e-09;
8; Mismatches 31
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86E9246E7680D81E CRC64;
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Indels Length

51;

Gaps

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91 197 ب 4.

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PREMARKATORY

QBLBV9

AC QBLBV9;

AC QBLBV9;

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Monodehydroascorbate reductase (NADH)-11ke protein.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;

OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;

C eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Search completed: January 29,
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Full-length cDNA from Arabidopsis thaliana.*;

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

-!- COFACTON: FAD (BY SIMILARITY).

REMBL; AY086968; AAM64531.1; -.

RINTEFFO; IPR00137; FAD pyr redox.

InterPro; IPR00137; FAD pyr redox.

InterPro; IPR001100; Pyr_redox.

R InterPro; IPR001100; Pyr_redox.

R Pfam; PF00070; pyr_redox; 1.

R PFINTS; PR00469; PNBTDTASEII.

R PRINTS; PR00469; PNBTDTASEII.

R PRINTS; PR00469; PNBTDTASEII.

R PRINTS; PR00461; PAD pyr_redox; 1.

PAD; Flavoprotein; Oxidoreductase.

SEQUENCE 434 AA; 46486 MM; ODBOC3FCF81D4COC CRC64;
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Best Local S
Matches 50
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Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;

"Full-length messenger RNA sequences greatly improve genome annotation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Brover V., Troukha
Feldmann K.;
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                                                                                                                                                                                                                                                           192 VFPEPWCMPRL--FTANIAAFYETYYTNKGVKIIKGTVASGFTAQPNGEVKEVQLKDGRT 249
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                                                                                                                                                                                                                                                                                                                                                                                         132 FGVKGADSKNILYLREIDDADKLVEAIKAKKGGKAVVVGGGYIGLELSAVLRINNLDVTM 191
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Minimum DB
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Perfect score:
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Result No.	Score	Query Query Match Length DB	ength	DB	ID	Description
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بر)	2788	100.0	544	23	AAU80330	Methylomonas 16a O
4	2008	72.0	542	22	AAU36340	Pseudomonas aerugi
ű	1916	68.7	5145 51	22	AAU34682	E. coli cellular p
6	1908.5	68.5	545	22	AAU35582	Haemophilus influe
7	1889.5	67.8	544	24	ABP76969	N. gonorrhoeae ami
œ	1783	64.0	511	22	AAU38272	Salmonella typhi c
9	1622.5	58.2	535	12	AAR15642	CTP synthetase. B

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prosoprita metanog Larval viability a Arabidopsis thalia	Human DITHP enzyme Human protein sequ	giedop	Arabidopsis thalia		olved	Lactococcus lactis	Protein involved i	Corynebacterium gl	C glutamicum prote	Lactococcus lactis	H. pylori cytoplas	Lactococcus lactis	Bifidobacterium lo	Lactococcus lactis	Helicobacter pylor	Streptococcus poly	Propionibacterium	Streptococcus poly		reptococcus	S. pneumoniae type	Streptococcus pneu	Enterococcus faeca		Staphylococcus epi		Staphylococcus aur	Staphylococcus aur	Listeria monocytog

ALIGNMENTS

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RESULT 1
ABG61.585
ID ABG6
XX ABG6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High growth methanotrophic bacterial strain; C1 carbon substrate; enzyme; methane; methanol; Embden-Meyerhof carbon flux pathway; 16s RNA; pyrophosphate dependent phosphofrutokinase; nitrogen-containing compound; ammonia; nitrate; nitrogen; pigment; oxygen; landfill; methane-containing environment; waste water treatment system; isoprenoid; nitrous oxide; terpenoid; animal feed; carotenoid; exopolysaccharide.
                                                                                                   Koffas M,
                                                                                                                                                                                                                                                                                                01-SEP-2000; 2000US-229858P
                                                                                                                                                                                                                                                                                                                                                                                              28-AUG-2001; 2001WO-US26827.
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                                                                                                   Schenzle A;
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N-PSDB; ABK83264

New high growth methanotrophic bacterial strain, useful for producing single cell proteins, grows on a Cl carbon substrate, and comprises a functional gene encoding in Embden-Meyerhof carbon pathway

Claim 11; Page 145-147; 157pp; English

The invention relates to a high growth methanotrophic bacterial strain, or which grows on a Cl carbon substrate e.g. methane and methanol, and comprises a functional Embden-Meyerhof carbon flux pathway comprising a gene coding a pyrophosphate dependent phosphofrutokinase enzyme or a 16s CR RNA. The bacterial strain is useful for the production of single cell crotein and for the bottransformation of a nitrogen-containing compound, e.g. ammonia, nitrate, nitrite or nitrogen. It is also useful for the production of a feed production of a feed production of a not requirement and for reducing oxygen demand, for removing nitrates and a CC pigment and for reducing oxygen demand, for removing nitrates and cC nitrites in methane-containing environments such as landfills, waste compared to the conversion of nitrate or nitrite to nitrous converse. The bacterial strain of the invention can be used as a converse of biomass including proteins, carbohydrates and a wide converse of pigments (particularly for isoprenoid pigments for the conversion of the production of terpenoid and composed of generating animal feeds), in production of terpenoid and computed, useful as pigments and as monomers in polymeric materials and in production of exopolysaccharides at high levels.

CC Sequences ABG61591 represent high growth methanotrophic conditions are constained to the invention. strain proteins of the invention.

Seguence 544 AA;

23;

Length

S 밁 g Ś Q 8 밁 Ś 8 멍 Ş da \$ B Ş g Query Match
Best Local Similarity
Matches 544; Conserv 481 421 421 361 361 301 301 241 181 181 121 121 61 ს ب VTEDGAETDIDLGHYERFIKITMTKKNNFTTGQVYEQVILRNERKGDYLGATVQVI PHITD 120 MTKFIFITGGVVSSLGKGIAASSLAAILEDRGLKVTITKLDPYINVDPGTMSPFOHGEVF EAAGMKFSGKSLDGRLVEIIBLPEHPWFLACQFHPEFTSTPRNGHALFSGFVEAAAKHKT EAGELVTRÐEDSDLGGTMRLGAQKCRLKADSLAFQLYQKDVITERHRHRYEFNNQYLKQL ISTVRFARENKIPYLGICLGMQSAVIEFARNVVGLEGAHSTEFLPKSPHPVIGLITEMMD TDAYKSLNEALIHAGIHTRHKVQISYIDSETIEAEGTAKLKNVDAILVPGGFGERGVEGK TDAYKSLNEALIHAGIHTKHKVQISYIDSETISAEGTAKLKNVDAILVPGGFGERGVEGK 360 DTIYRIPLLLREQGLDDLVVDQLRLDVPAADLSAWEXVVDGLTHPTDEVSIAIVGKYVDH SAGELKTKPTQHSVKELRTIGIQPDILICRSEQPIPASERRKIALFTNVAEKAVISAIDA SAGELKTKPTQHSVKELRTIGIQPDILICRSEQPIPASERRKIALFTNVAEKAVISAIDA EIKRRYTESAEGKDVALIEVGGTVGDIESLPFLETIRQMGVELGRERALFIHLTLVPYIK EIKRRYESAEGKOVALIBYGGTYGDIESLPFLETIRQMGVELGRORALFIHLTLVPYIK VTSDGABTDLDLGHYERFLKTTMTKKKNNFTTGQVYEQVLRNERKGDYLGATVQVIPHITD MTKFIFITGGVVSSLGKGIAASSLAAILEDRGLKVTITKLDPYINVDPGTMSPFQHGEVF DTIYRIPLILREQGLDDLVVDQLRLDVPAADLSAWEKVVDGLTHPTDBVSIAIVGKYVDH Conservative 100 .0%; Score 2788; DB 2 .0%; Pred. No. 3e-248; 0 Mismatches .. Indels 0 Gaps 180 300 180 60 60 540 420 420 960 300 240 240 120 480

> RESULT 2
> AABZ23366
> ID AABZ23366
> ID AABZ23366
> ID AABZ23366
> ID XX AABZ
> X 맑 Carotenoid; isopentenyl pyrophosphate; antheraxanthin; astaxanthin; diet; anti-oxidant; steroid; flavour; fragrance; electro-optic application; aquaculture; enzyme; CTP synthase; PyrG. 04-SEP-2001; 07-MAR-2002 WO200218617-A2 Methylomonas 16a AAB22306; AAE22306 standard; Protein; 544 541 QGTA 16a sp. 2001WO-US27420 544 (first ďŝ CTP synthase (PyrG) enzyme 3

Brzostowicz PC, Chen Odom JM, Picataggio 01-SEP-2000; 01-SEP-2000; N-PSDB; (BURO) 2002-351711/38. PONT DE NEMOURS 2000US-229858P. 2000US-229907P. Cheng Q, aggio SK, Rouviere Ŗ٦ Dicosimo DJ, Rouviere PE; S Koffas z,

Miller

E S

Producing carotenoid compounds e.g. antheraxanthin and astaxanthin, by using microorganisms having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolize single carbon substrates 'n

Claim 46; Page 120-122; 156pp; English

The method comprises a transformed metabolising host cell, comprising suitable levels of isopentenyl pyrophosphate and a nucleic acid molecule encoding an enzyme in the carocenoid biosynthetic pathway, under the control of regulatory sequences, and contacting the host cell with carbon substrate to produce a carotenoid compound. The method is useful for producing carotenoid compounds anther exanthin and astaxanthin, by using microorganism having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolise single carbon substrates. The carotenoids have potent anti-oxidant properties useful in diet, and aquaculture elements. The carotenoids are also useful as intermediates in the synthesis of steroids flavours and fragrances and compounds for potential electro-optic applications. The present sequence is Methylomonas 16a sp. CTP synthase (PyrG) enzyme used in the invention.

Sequence 544 Ä

5 밁 ₽ S Query Match Best Local S Matches 544 544 61 μ Similarity VTEDGAETDLDLGHYERFLKTIMIKKNNFTIGQVYEQVLRNERKGDYLGATVQVIPHIID MTKPIFITGGVVSSIGKGIAASSLAAILEDRGLKVTITKLDPYINVDPGTMSPPQHGEVF MTKF1F1TGGVVSSLGKG1AASSLAA1LEDRGLKVT1TKLDPY1NVDPGTMSPFQHGEVF Conservative 100.0%; 0; Score 2788; DB 2 Pred. No. 3e-248; Mismatches 23; 0 Indels Length 544; 0; 120 120 60 60

61

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RESULT 3
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ID AAUB
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The present invention relates to a new nucleic acid molecule encoding an isoprenoid biosynthetic enzyme isolated from Methylomonas 16a.
                                       Claim 4; Page 74-76; 84pp; English
                                                                       compounds
                                                                                   Novel nucleic acid molecule encoding a isolated from Methylomonas 16a, useful
                                                                                                                             N-PSDB;
                                                                                                                                                                    Cheng Q, Ko
Schenzle A,
                                                                                                                                                                                                                                                                                                                                                          Methylomonas sp
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pyrG; CTP sy
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Best Local Similarity
Matches 544; Conserv
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14-FEB-2002
                            AAU36340;
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                                  Protein;
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aeruginosa cellular proliferation protein, protein

Antisense; prokaryotic cellular proliferation antibiotic; antibacterial; drug design.

Pseudomonas aeruginosa

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CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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Best Local S
Matches 383
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23-MAY-2000;
26-MAY-2000;
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27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
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DB; AAS54199.
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                                                                                                                                                                                                                                                                                                             Similarity
                    DTIYRIPLLLREQGLDDLVVDQLRLDVPAADLSAWEKVVDGLTHPTDEVSIAIVGKYVDH
                                                                                                                                        EIKRRYYESAEGKDVALIEVGGTVGDIESLPFLETIRQMGVELGRDRALFIHLTLVPYIK
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DTIXRIPSVLHAQGLDDIVVERFGLECGQADLSEWDRVVDAKLNPEREVTIAMVGKYMEL
                                                                                     SAGELKTKPTQHSVKELRTIGIQPDILICRSEQPIPASERRKIALFTNVAEKAVISAIDA
                                                                                                                   EIKRRIIKGAGDADVALVEIGGTVGDIESQPFLEAIRQLRVEIGAKRAMLMHLTLVPYIA
                                                                                                                                                                           VTQDGAETDLDLGHYERFVRTTMTQNNNFTTGRVYMDVLRKERRGDYLGATVQVI PHITD
                                                                                                                                                                                                VTBDGAETDLDLGHYERFLKTTWTKKNNFTTGQVYEQVLRNERKGDYLGATVQVIPHITD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq ID No 11933; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                         542 AA;
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2000US-206848P.
; 2000US-207727P.
; 2000US-242578P.
; 2000US-257931P.
; 2000US-257931P.
; 2000US-269308P.
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Xu HH;
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Pred. No. 3e-176;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are scherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Entercocccus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense mucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense mucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in

New polynucleotides for the identification and antibiotics, comprise sequences of antisense nu

nucleic acids

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Example 3; Seq ID No 10275; 511pp; English

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23-MAY-2000;
26-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
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)B; AAS52541.
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2000US-20684BP.

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Best Local S
Matches 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a wide variety of organisms. The present sequence represents essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
21-MAR-2000; 2000US-191078P.
23-MAY-2000; 2000US-206848P.
                          21-MAR-2001;
                                                               WO200170955-A2
                                                                                                   Antisense; prokaryotic cellular proliferation antibiotic; antibacterial; drug design.
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                                                                                                                               Haemophilus
                                                                                                                                                                                      AAU35582 standard;
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ed. No. 9.3e-168;
Mismatches 102;
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364;

Conservative

Similarity

68.5%;

; Score 1908.5; DB 22; ; Pred. No. 4.6e-167; 71; Mismatches 103; I

Indels Length

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545;

363 362 303 302

STVRFARENKIPYLGICLGMQSAVIEFARWVVGLEGAHSTEFLFKSPHPVIGLITEWMDE 421

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182 123 122

63 62 w N

TEDGAETDLDLGHYERFLKTYMYKKNNFTTGQVYEQVLRNERKGDYLGATVQVIPHITDE 121

TKFIFITGGVVSSLGKGIAASSLAAILEDRGLKVTITKLDPYINVDPGTMSPFQHGEVFV

INYIFVIGGVVSSLGKGIAAASLAAILEARGLNVTIMKLDPYINVDPGTMSPTQHGEVFV 62

243 242

SIYQIPALLKSQGLDDFYCERFRLTCPEADLTEMBQYLXXQANPYGEYTIGMVGXYTELP

DAYKSLNEALIHAGIHTRHKVQISYIDSETIEAEGTAKLKNVDAILVPGGFGERGVEGKI

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182

DAYKSVNEALKHAGLTNRLSVNIKYIDSQDVETKGVEVLKGIDGILVPGGFGYRGVEGKI

TIYRIPLLLREQGLDDLVVDQLRLDVPAADLSAMEKVVDGLTHPTDEVSIAIVGKYVDHT 301

AGEVKTKPTQHSVKELLSIGIQPDVLICRSDRMIPPNERAKIALFCNVAERAVISLKDVN AGELKTKPTQHSVKBLRTIGIQPDILICRSEQPIPASBRRKIALFTNVABKAVISAIDAD 241 IKDRVIAGAQGHDVVIVEVGGTVGDIESLPFLEALRQLAVQVGREHTLFMHLTLVPYIPT IKRRVYBSABGKDVALIEVGGTVGDIBSLPFLETIRQMGVELGRDRALFIHLTLVPYIKS 181 TODGAETDLDLGHYERFIRTKWIKRNNFTTGKIYSEVLRKERRGDYLGATIQVIPHITNE 122

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The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery corresponds mucleic acids which are required for cell proliferation in cessential prokaryotic cellular proliferation protein.

CC wide variety of organisms. The present sequence represents an cessential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WiPO at
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23-OCT-2000;
27-NOV-2000;
27-DSC-2000;
16-FEB-2001;
Sequence
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Yamamoto RT,
                                                ftp.wipo.int/pub/published_pct_sequences.
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   545 AA;
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; 2000US-253625P.
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Best Local S
Matches 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP76736-ABP81046 represent nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins a antibodies that specifically bind to the proteins. The composition
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AAGEIKTKETQHTVKEMLSIGLQEDILICRMDRKMEADERRKIALECNVEERAIVGSYDV
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Pred. No. 2.6e-165;
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Yamamoto RT,
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella

No 13865; 511pp;

English

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RESULT 9
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Best Local (
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              Bacillus natto
                                         Cytidine
                                                                 CTP synthetase
                                                                                              25-MAR-2003
05-FEB-1992
                                                                                                                                    AAR15642;
                                                                                                                                                              AAR15642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acids sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                            standard;
                                                                                                                                                                                                                                             AAGMKPSGKSLDGRLVEIIELPEHPW 507
                                                                                                                                                                                                                                                                                                                                      ATARYARENNIPYLGICLGMQVALIEFARNVAGMDNANSTEFVPDCKYPVVALITEWRDE
                                                                                                                                                                                                                                                                                                                                                             STVRFARENKIPYLGICLGMQSAVISFARNVVGLEGAHSTEFLPKSPHPVIGLITEWMD8
                                                                                                                                                                                                                                                                                                                                                                                                                    DAYKSLNEALIHAGIHTRHKVQISYIDSETIEAEGTAKLKNVDAILVPGGFGERGVEGKI
                                                                                                                                                                                                                                                                                                                                                                                                                                              SIYKIPGLLKSQGLDDYICKRFSLNCPEANLSEWBQVIYEEANPAGEVTIGMVGKYIELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIYRIPLLLERGGLDDLVVDQLRLSVPAADLSAWSKVVDGLTHPTDEVSIAIVGKYVDHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGNVBVRSEKSDLGGTMRLGAQQCQLSDDSLVRQLYGASTIVERHRHRYEVNNMLLKQIB
                                                                                                                                                                                                                                                                                                  AGELVTRDEDSDLGGTMRLGAQKCRLKADSLAFQLYQKDVITERHRHRYEFNNQYLKQLZ
                                                                                                                                                                                                                                                                                                                                                                                         DAYKSVIEALKHGGLKNRVTVNÍKLÍDSQÐVETRGVEILKDLDAILIPGGFGYRGVEGKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGELKTKPTQHSVKELRTIGIQPDILICRSEQPIPASERRKIALFTNVABKAVISAIDAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGXXXXGRSGDDQLVEIIEVPNHXW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGEVKTKPTQHSVKELLSIGIQPDILICRSDRAVPANERAKIALFCNVPEKAVISMKDVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKRRYYSSAEGKDVALIEYGGTYGDIESLPFLETIRQMGVELGRDRALFIHLTLVPYIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 511 AA,
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                                                                                           (updated)
(first en
                                                                                                                                                            Protein;
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; Pred. No. 1.6e-155;
64; Mismatches 101;
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Best Local |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prodn. of cytidine by fermentation with increased yield - transforming a suitable microorganism with a recombinant I CTP synthetase gene and incubating with a uracil cpd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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Similarity 57.0%;
AANO
                          HKTQ 541
                                                                    KQLEAAGMKFSGKSLDGRLVEIIELPEHPWFLACQFHPEFTSTPRNGHALFSGFVEAAAK 537
                                                                                                   QKDV------EDIGGTLRLGLYPCKLEEGTKAFEVYQDEVVYERHRHYEFNNEFR 470
                                                                                                                    WWDEAGELVTRDEDSDLGGTMRLGAQKCRLKADSLAPQLYQKDVITERHRHRYEFNNQYL 477
                                                  QMEEQGFVFSGTSPDGRLVEIIELKDHPWFVASQFHPEFKSRPTRPQPLFKGFIGASVB
                                                                                                                                                                                                             ELPDAYISVVESLRHAĞYAFDTDVKVKWİNAEEVTENNI AELTSGTDGI IVPGGFGDRGV
                                                                                                                                                                                                                                                              DADNIYSIPLELQKQGLDKLVCEHMXLACKEAEMSEWKELVNKVSNLSQTITIGLVGKYV
                                                                                                                                                                                                                                                                                                                                                                                           EIKRRYYESAE--GKDVALIEVGGTVGDIESLPFLETIRQMGVELGRDRALFIHLTLVPY 178
                                                                                                                                                                                                                                                                                                                                                                                                                          VTDDGAETDLDLGHYERFIDINLNKFSNVTTGKIYSTVLKKERRGDYLGGTVQVIPHITN
                                                                                                                                                                                                                                                                                                                                                                                                                                        VTEDGAETDLDLGHYERFLKTTMTKKNNFTTGQVYEQVLANERKGDYLGATVQVIPHITD 120
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                                                                                                                                                          BGKIVATKYARENNIPFLGICLGMQVASIEYARNVLGLKGAHSABIDPSTQYPIIDLLPE 420
                                                                                                                                                                         EGKISTVRFARENKIPYLGICLGMQSAVIEFARNVVGLEGAHSTEFLPKSPHPVIGLITE 417
                                                                                                                                                                                                                                    DHTDAYKSLNEALTHAGIHTRHKVQISYIDSETIEAEGTAKL-KNVDAILVPGGEGERGV 357
                                                                                                                                                                                                                                                                                      DADTIYRIPILLREQGLDDLVVDQLRLDVPAADLSAWEKVVDGLTHPTDEVSIAIVGKYV 298
                                                                                                                                                                                                                                                                                                                    IKAAGELKTKPTQHSVKELRSLGIQPNIIVVRTEMPISQDMKDKIALFCDIDTKAVIECE
                                                                                                                                                                                                                                                                                                                                  IKSAGBIKTKPTQHSVKBLRTIGIQPDILICRSBQPIPASERRKIALFTNVABKAVISAI 238
                                                                                                                                                                                                                                                                                                                                                                       BLKDRYYRAGKETNADVVITEIGGTVGDIESLPPLEAIROMKSDIGRENVMYIHCTLVPY
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534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94;
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Pred. No. 1.1e-140;
Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12; Length
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RESULT 10 ABB48439 ID ABB48

ABB48439

standard;

Protein;

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                                                                                                                                                                                                                                                                                                                            The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms.

Note: The sequence data for this patent did not form part of the printed sepeciation, but was obtained in electronic format directly from WIPO as firm with out the parameters.
                                                                                                                                                                                                 Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chakraborty T, Domann E, Perez-Diaz J, Baquero F, Maduenio E, De Pablos B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200177335-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-2000; 2000FR-0004629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Listeria monocytogenes protein #1143
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                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                 299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptides
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EIKRRVYESAE--GKDVALIEVGGTVGDIESLPFLETIRQMGVELGRDRALFIHLTLVPY 178
                                                        VTEDGAETDLDLGHYERFLKTTMTKKUNFTTGQVYEQVLRNERKGDYLGATVQVIPHITD 120
                                                                                                                 MTKY1FVTGGVVSS1GKG1TAASLGRLLKNRGLSVT1QKFDPY1NVDPGTMSPYQHGEVY
                                                                                                                                         MTKFIFITGGVVSSLGKGIAASSLAAILEDRGLKVTITKLDPYINVDPGTMSPPQHGEVF
                                     VTDDGAETDLDLGHYERFIDINLNKYSNVTTGKVYSEVIKKERRGDYLGGTVQVIPHITN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C, Frangeul L, Couve B, Rusniok C, Fsihi H, Dehoux P, O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Goebel W, Kreft J, Kahn M, Ng E, Vazquez-Boland JA, Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; YT, Domann E, Hain T, Berche P, Charbit A, Durant L; J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                             532
                                                                                                                                                                                               Conservative

    gene therapy; vaccine; biosynthesis; biodegradation;
bacterial infection; disease.

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                                                                                                                                                                                         57.4%; Score 1600.5; DB 23; Lengt 55.2%; Pred. No. 1.2e-138; tive 104; Mismatches 126; Indels
                                                                                                                                                                                                                                 Length
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RESULT 11
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ID AAU36
AX AAU36
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23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
22-DBC-2000; 2000US-253625P.
16-FEB-2001; 2001US-269308P.
                                                                                                                                                                                                      Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids ${\bf r}$

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Example 3; Seq ID No 12372; 511pp; English

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RESULT 12
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CC Note: The sequence data for this patent did not form part CC from this pacint did not form part contains the printed specification, but was obtained in electronic
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at
                                                                                                                                                                                       Matches 302;
                                                                                                                                                                                                         Query Match
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
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N-PSDB; AAS55244.
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                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2001; 2001WO-US09180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus cellular proliferation protein #1555
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                                                                                                                                                                                                           Similarity
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EIKRRYYBSAE--GKDVALIEVGGTVGDIESLPPLETIRQMGVELGRDRALFIHLTLVPY
                                                  VIDDGAETDLDLGHYBRFIDINLNKFSNVTAGKVYSHVLKKBRRGDYLGGTVQVIPHITN
                                                                   VTEDGAETDLDLGHYERFLKTTMTKKNNFTTGQVYEQVLRNERKGDYLGATVQVIPHITD 120
                                                                                                                    MTKFIPVTGGVVSSLGKGITASSLGRLLKORGLAVTIQKFDPYLAVDPGTMSPYQHGEVF
                                                                                                                                                    MTKFIFITGGVVSSLGKGIAASSLAAILBDRGLKVTITKLDPYINVDPGTMSPFQHGEVF
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2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
                                                                                                                                                                                        Conservative
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Xu HH;
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                                                                                                                                                                                        93;
                                                                                                                                                                                                       Score 1576; DB 22;
Pred. No. 2.2e-136;
                                                                                                                                                                                        Mismatches 134;
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                                                                                                                                                                                        Indels
                                                                                                                                                                                                                         Length 536;
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  AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (III), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the 5 epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
                                                                                                                                                                                                                            Claim
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                                                                                                                                                                                                                                                                          cacids encoding polypeptides from Staphylococcus epidermidis, for vaccinating against infections, e.g. endocarditis -
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N.B. The present invention specifically claims all the polymucleotide sequences given in the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4465 to 4472,
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                                                              REQLESNGMVFSGTSPDGRLVEIIEIPKNDFFIACQFHPEFLSRPNRPQPIFKSFVEAAL
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Pred. No. 2.7e-136;
95; Mismatches 132;
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ABP39346 standard; Protein;

561

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ABP39346;

24-JUL-2002 (first entry)

Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4191.

RBSULT 14
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N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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08-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
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                                                                     VEGKISTVRFARENKIPYLGICKMOSAVIEPARNVVGLEGAHSTEPLPKSPHPVIGLIT 416
                                                                                                                                     VDHTDAYKSLNEALIHAGIHTRHKVQISYIDSETIBABGT-AKLKNVDAILVPGGFGERG
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                       EWMDEAGELVTRDEDSDLGGTMRLGAQKCRLKADSLAFQLYQKDVITERHRHRYEFNNQY
                                                                                                                  VSLQDAYLSVVESLKHAGYPFKKDVVVKWIDSSEVNDDNVEAYLSDVDGILVPGGFGFRA
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97US-064964P.
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- I EDLGGTLRLGLYPCHI KEGTLAEKI YNKND I BERHRHRYE FNNEF
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                                          invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                  genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
                                                                                                                                                                                                                                                                                                 The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the
                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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23-MAY-2000;
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N-PSDB; AAS51347.
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16-FEB-2001;
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23-OCT-2000;
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                            ftp.wipo.int/pub/published_pct_sequences
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2000US-242578P.
2000US-253625P.
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                                                              531 ANK 533
                               471 RQLFEENGLVFSGVSPDNRLVEIVEIPEKQFFVACQFHPELISRPNRPQRLIKGFVGAAL 530
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Search completed: January 29, 2004, 15:49:45
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length: 20000000000
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| Cgm2_6/ptodata/1/iaa/5A_COME.pep:*
| Cgm2_6/ptodata/1/iaa/5B_COME.pep:*
| Cgm2_6/ptodata/1/iaa/6A_COME.pep:*
| Cgm2_6/ptodata/1/iaa/6A_COME.pep:*
| Cgm2_6/ptodata/1/iaa/6B_COME.pep:*
| Cgm2_6/ptodata/1/iaa/backfIles1.pep:*
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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US-09-134-001C-4191
US-09-1198-452A-246
US-09-107-532A-4108
US-09-107-532A-4108
US-09-107-532A-5709
US-09-107-532A-5709
US-09-107-532A-5709
US-09-116-098-2
US-09-252-991A-27277
US-08-687-590-32
US-09-252-991A-32742
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US-09-252-991A-16679
US-09-252-991A-1679
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US-09-252-991A-324-610
US-09-252-991A-3528-610
US-09-252-991A-3528-610
US-09-252-991A-3528-610
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7224, App
4191, Ap
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4109, Ap
4109, Ap
4109, A
5709, A
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72277, A
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US-09-252-991A-21120
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GENERAL INFORMATION: APPLICANT: Marc J Ru TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
TITLE REPERENCE: 10719
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Sequence	US-09-255-829-20	4	1169	3.6	99.5	
Sequence	US-09-252-991A-32974	4	921	3.6	99.5	
Sequence	US-09-255-829-29	4	858	3.6	99.5	
Sequence	US-09-255-829-22	4.	858	3.6	99.5	
Sequence	US-09-252-991A-24209	4	551	3.6	99.5	
Sequence	US-09-252-991A-27783	4	524	3.6	99.5	
Sequence	US-09-322-478-18	41	1802	3.6	100	
Sequence	US-09-252-991A-24495	44	1044	3.6	100	
Sequence	US-08-804-198-4	N	3724	3.6	100.5	
Sequence	US-08-804-227C-10	N	3724	з. 6	100.5	
Sequence	US-08-840-006-5	w	1200	3.6	100.5	
Sequence	US-08-840-006-6		1151	3.6	100.5	
Sequence	US-09-252-991A-26782		582	3.6	100.5	
Sequence	US-07-603-133B-13	1~1	775	3.6	101	
Sequence	US-09-594-185-2	44	236	3.6	101	
Sequence	US-08-935-263-2	w	236	ы. 6	101	
Sequence	US-09-198-452A-610	,D.	458	9. 6	101.5	
Sequenc	US-08-446-137B-2	w	1027	3.7	102	

ALIGNMENTS

US/09252991A

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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21120
LENGTH: 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                         MTKFIFITGGVVSSLGKGIAASSLAAILEDRGLKVTITKLDPYINVDPGTMSPFQHGEVF
LDAYKSLIEAMTHAGIQSRTKVNLRYIDSEDIEQQGTSLLEGVDAILVPGGFGLRGVEGK
                       TDAYKSLNEALIHAGIHTRHKVQISYIDSETIEAEGTAKLKNVDAILVPGGFGERGVEGK
                                                                                                          DTIYRIPLLLREQGLDDLVVDQLRLDVPAADLSAWEKVVDGLTHPTDEVSIAIVGKYVDH 300
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                                                                                       DTIYRIPSVLHAQGLDDIVVERFGLECGQADLSEWDRVVDAKLNPEREVTIAMVGKYMEL
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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71.2%;
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Pred. No. 2.4e-188;
3; Mismatches 92;
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GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7224
LENGTH: 567
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-7224
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US-09-328-352-7224
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Best Local S
Matches 351
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Patent No. 6562958
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                                                        AIEQAGMKISGYSSAQHLVETVEIPEHPWFIAVQFHPEFTSSPRDGHPLFASFIDAA---
                                                                                                                               LDERGELQQRSLESDLGGTMRLGAQKSELVEGTKTREVYGKAEITERHRHRYEMNNRFIE
                                                                                                                                                    MDEAGELVTRDEDSDLGGTMRLGAQKCRLKADSLAFQLYQKDVITERHRHRYEFNNQYLK
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; Pred. No. 9.3e-171;
81; Mismatches 106;
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CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4191
LENGTH: 561
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4191
RESULT 4
US-09-198-452A-246
; Sequence 246, Application US/09198452A
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US-09-134-001C-4191
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Best Local (
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                                                                                                                                                                                    LKQLEAAGMXFSGKSLDGRLVBIIELPBHPWFLACQFHPBFTSTPRNGHALFSGFVEAAA 536
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RESULT 5
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                                                                                                                                                                      Sequence 6925, Application US/09107532A
PATENT NO. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6559294

APPLICANT: Griffals, R.
APPLICANT: Griffals, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, frag
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis,
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT PILING DATE: 1938-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 246
LENGTH: 537
TYPE: PRI
ORGANISM: Chlamydia pneumoniae
ORGANISM: Chlamydia pneumoniae
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                                                                         NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESSE: CENOME THERAPEUTICS
STREET: 100 Beaver Street
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                STATE: Massachusetts COUNTRY: USA
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                                                      STREET: 100 B
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50.5%; Pred. No. 1.5e-124;
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AND AMINO ACID SEQUENCES REL
FAECIUM FOR DIAGNOSTICS AND
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NAME/KEY: misc_feature
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LOCATION: (B) LOCATION 1...3
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SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-107-532A-6925
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US-09-107-532A-4108
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          Sequence 4108, Application US/09107532A
Sequence 4108, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION: DOucette-Stamm
APPLICANT: LYDD A DOUCETIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity Matches 197; Conserv
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APPLICATION NUMBER: US/09/107,532A
PRILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNSY/AGENT INFORMATION:
  NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAMÉ: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
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OPERATING SYSTEM: <Unknown>
SOPTWARE: ASCII
                                                                                                                                                                                                                                                                                                  DVDTLYSIPLVLQAQGMDQIVCDHLKLDTPEADMTEWKELEERVLNLKKKVRIALVGKYV 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 340 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.3%; Score 1039; DB 4; 59.2%; Pred. No. 9.7e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTC-012
                  and David Sush
AND AMINO ACID SEQUENCES RELATING TO
REPARCIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6925:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 340;
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12:

Gaps

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US-09-252-991A-25369
; Sequence 25369, Application US/09252991A
; Patent No. 6551795
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                    GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
CURRENT APPLICATION NUMBER: US/09/252,991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (781)893-8277 INFORMATION FOR SEQ ID NO: 4108:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELEPRONE: (781)893-5007
TELEPRONE: (781)893-5007
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Umn-1998
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/RO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...226
SEQUENCE DESCRIPTION: SEQ ID NO: 4108:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                          175
                                                                                                                                                                                                                                                                                                                                                                                115 ENLGGTIRLGLYPCKIKKGTKTAEAYGGADVVQERHHHYEFNNKYRQLFEEQGLVFSGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110;
                                                                                                                                                                                                                                                                                                                                                                                                                                 432 SDLGGTWRLGAQKCRLKADSLAFQLY-QKDVITERHRHRYBFNNOYLKQLBAAGNKFSGK 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372 IPYLGICLEXQSAVIEFARNVVGLEGAHSTEFLPKSPHPVIGLITEMMDEAGELVTRDED 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313 HAGIHTRHKVQISYIDSETIEAEGT-AKLKNVDAILVPGGFGERGVEGKISTVRFARENK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 VPFLGICLGMQMACVEFARNVVGLEDASSABTNPDTANNIIDLMAD------QENI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                     SPDNRLVBIVBLPEKKPFVGCQFHPELISRPNRPQKLIKAFVGASLADHETK 226
                                                                                                                                                                                                                                                                                                                      SLDGRLVEIIELPEHPWFLACQFHPEFTSTPRNGHALFSGFVEAA-AKHKTQ 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSGFAYNSDIEIDWIKAQELTRENVEERLKDADGILVPGGFGDRGVEGKIEAIRYAREND 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 Beaver Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 544.5; DB 4;
Pred. No. 2.2e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 226;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
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LENGTH: 373
; TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5709, Application US/09107532A
Parent No. 6583275
PARENT INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity es 72; Conserv
                                                                                                                                   APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02354
COMPUTER REALABLE FORM:
MEDIUM TYPE: CD/ROM IS09660
                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 7310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283 THPTDEVSIAIVGKYVDHTDAYKSLNEALIHAGIHTRHKVQISYIDSETIEAEGTAKLKN 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343 VDAILVPGGFGERGVEGKISTVRFARENKIPYLGICLGKOSAVIEFARNVVGLEGAHSTE 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                 COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLPPLPKAFVEAC --- RTQ 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGHALFSGFVEAAAKHKTQ 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TERHRHRYEFNNQYLKQLEAAGMKFSGKSLDGRLVEIIELPEHPWFLACQFHPEFTSTPR 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLPKSPHPVIGLITEWMDEAGBLVTRDEDSDLGGTMRLGAQKCRLKADSLAFQLYQKDVI 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPPAAPLRIALVGDHDPHITAHRAIPLALRLAGEALGLEIAFDWLASDRLPAE--PALER
                                                                         NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDGFWCVPGSPYRDADAVLRLIAHARGRRRPFLGTCAGFQHTILEFARNALGWQAATHGE 137
TELEPHONE: (781,000)
TELEPHONE: (781,893-8277)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EADYHCRYAIAPRFAABLTGGALRASAWSADG-AIRAVELEQHPFFVATLFQPBRAAVAG
                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 100 Beaver Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENOME THERAPEUTICS CORPORATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUT
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RESULT 9
US-09-252-991A-27277
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                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: ARRUGINGS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
TOTALO OF THE REFERENCE: 107196.136
                                                                                                                                                                                             Sequence 27277, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 115; Conserv
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 5709:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...830
SEQUENCE DESCRIPTION: SEQ ID NO: 5709:
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                                                                                                                                                                                                                                                                                                                                     DHKAMOKRILEE----LKKAFRPEF 715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVISFARNVVGLEGAHSTEFLPKSPHPVIGLITEWNDBAGELVTRDEDSDLGGTMRLGAQ 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --IDESAAKVRLDQTDHLTKS-TVIKLEIDELVQEKEAAIQKQD-----FENAAQLRRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPYIKSAGELKTKPTQHSVKELRTIGIQPDILICRSEQPIPASERRKIALFTNVA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AETOLOLGHYERFLKTTMTKKNWFTTGQV----YEQVLRNERKGDYLGATVQVIPHITDE
                                                                                                                                                                                                                                                                                                                                                                             DGRIVEIIELPEHPWFLACQFHPBF 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETISAEGTAKIKNVD-----AILVPGGFGERGVEGKISTVRFARENKIFYLGICLGMQS 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKESERLLELEGLLHE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKALRKKLQKVSAIBAK---
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                          KAHPDVFNLLLQVLDDGHLTDSKGRKVDFRNTIMIMISNIGATQIREEKNVGFNVQDVTK 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KCRLKADSLAFQLYQKDVITERHRHRYEFNN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.4%; Score 123.5; DB 4; ilarity 20.4%; Pred. No. 0.0051; Conservative 80; Mismatches 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----RVVGQDEAVKAVSRAIRRA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----QYLKQLEAAGMKFSGKSL 492
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US-08-116-098-2
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US-09-252-991A-27277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27277
LENGTH: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 2, Application US/08116098
Patent No. 5428131
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Trent, Jonathan D.
APPLICANT: Horwich, Arthur L.
TITLE OF INVENTION: Archaebacterial Chaperonin-Mediated
TITLE OF INVENTION: Protein Stabilization
                                                                                   CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
APPLICATION NUMBER: US 07/756627 FILING DATE: 09-SEP-1991 APPLICATION NUMBER: US 07/721974 FILING DATE: 27-JUN-1991
                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                        CITY: Atlanta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALASGAKTLKMGHGHHGAN-----HPV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVPAQTPASEVLA--LNPDGIFLSNGPGDPEPCDYAIQAIREFLDTEIPVFGICLGHQLL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YIDSETIEAEGTAKLKNVDAILVPGGFGE-RGVEGKISTVRFARENKIPYLGICLGWQ-S 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHIGNIG---TIPEDAEANRVWAAG-----LIIRDLPLIASNWRSKQSLPDYLKANGTVA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NHGFAVDESTL----PDNLRATHKSLFDGTLQGIERTDKVAFSFQG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVIEFARNIVIGLEGAHSTEFLEKSPHEVIGLITEWMDEAGELVTRDEDSDLGGTWRLGAQ 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYIKSAGELKTKPTQHSVKELRTIGIQPDILICRSEQPIPASERRKIALFTNVAEKAVIS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KCRLKADSLAFQLYQXDVITERHRHRYEFNNOYLKQLEAAGMKFSGKSLDGRLVEIIBLP 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EWRSSVWNLESDSHP--EIP---AGELPYHVVAYDYGVKLNILRMLVARG-----CRLS 240
                                                                                                                                                                                                                                                                                                                                                 Georgia
                                                                                                                                                                                                                                                                                                                                                                                               1100 Peachtree Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----LVVDQLRLDVPAADLS 273
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US-08-116-098-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE:
ORIGINAL SOURCE:
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HYPOTHETICAL: N
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LENGTH: 552 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Pabst, Patrea L. REGISTRATION NUMBER: 31 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 24-OCT
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APPLICATION NUMBER: US 0
PILING DATE: 18-MAR-1991
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499 IIELPEHPWFL 509
                                                                                                                                                                                                 332 RATGGRVISNIDBLTSQDLGYAALVEERKVGEDKWVFVEGAKN----PKSVSILIRGGLE 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 NVAEKAVISAIDADTIYRIPLLLREQGLDDLVVD-----QLRLDVPAADLSAWE--KVV 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126
                                                                                                                                                                                                                                                                                                                                                                                                   280 DGLTHPTDEVSIAIVGKYVDHTDAYKSLNEALIHAGIHTRHKVQISYIDSET-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 HLT-LVPYIKSAGELKTKPTOHSVKELRTIGIQPDILICRSEQPIPASER----RKIALFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 VQVIPHITDEIKRRVYESAEGKDVALIEVGGTVGDIESLPFLETIRQMGVELGRDRALFI 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 ---GDITITNDGATILDKMDLQH-------PTGKLLVQIAKGQ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 IFITGGVVSSLGKGIAASSLAAI--LED-----RGL-KVTITKLDFYINVDFGTMSF 53
                                                                                                                                                                                                                                                                                                                    ---IEAEGTAKLKNVDAILVPGG---FGERGVE-----GKISTVRFARENKIPYLG
                                    ANAI EGLIMI LAENAGLDPI DKLMQLRSLHENETNKWYGLNL----FTGN---
                                                                                QKOV---
                                                                                                                  RVVDET-ERALRDALGTVADVIRDGRAVAGGGAVEIEIAKRLRKYAPQVGGKEQLAIEAY 446
                                                                                                                                                           EWMDEAGELVTRDEDSDLGGTMRLG-----
                                                                                                                                                                                                                                                                              HKFLEEERNILKEKVDKIAATGANVVICQKGIDEVAQHYLAKKGILAVRRAKKSDLEKLA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLGSKAVAGA-----
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                                                                                                                                                                                                                                                                                                                                                             GGSINDTQLVYGIVVDKEVVHPGMPKRIENAKI-ALLDASLEVEKPELDAEIRINDPTQM 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IILKEGSSRTYGKEALRANIAAVKAIEEALKSTYGPRGMDKMFVDSL-------
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Conservative 73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -ETADGTKTAVILAGELAKKAEDLLYKE-----
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                                                                            -ITERHRHRYEFNNOYLKQLEAAGMKFSGKSLDGRLVE 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----DI----AQPVSINDTDVLRKVAL-T
                                                                                                                                                         -----AQKCRLKA-----DSLAFQLY 457
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US-08-687-590-32
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GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: GB 9
FILING DATE: 31-JAN-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Iwo
CITY: San Francisco
STATE: California
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 31-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                          Local 129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NO. 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: GB 9418234.2 FILING DATE: 09-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/687,590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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 SLGSKAVAGA-
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                                                                                                                                                                                                                                                         IILKEGSSRTYGKEALRANIAAVKAIEEALKSTYGPRGMDKMFVDSL-
                                                                                             HLT-LVPYIKSAGELKTKPTQHSVKELRTIGIQPDILICRSEQPIPASER----RKIALFT 227
                                                                                                                            -----DE----ETADGTKTAVILAGELAKKAEDLLYKE-----I
                                                                                                                                                                                                                                                                                        IFITGGVVSSLGKGIAASSLAAI--LED-----RGL-KVTITKLDPYINVDPGTMSP 53
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Two Embarcadero Center, Eighth Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        552 amino acids
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Willison, nu.
Nota, Hiroshi
Nlan
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Ashworth, Folding Proteins
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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-REYLADIVVKAVAQVABLRGDKWYVDLDNVQIVKKH
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                                                              -AQPVSINDTDVLRKVAL-T
                                                                                                                                                                                                                                                                                                                                                       Length 552;
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RESULT 12
US-09-066-046-2
; Sequence 2, Application US/09066046A
; Patent No. 6204252
; GENERAL INFORMATION:
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-066-046-2
                                                                                                                                                                               TELEPAX: (617) 526-5
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
REPLICATION DATA:
APPLICATION UNMBER: US/09/066,046A
FILING DATE: 24-Apr-1998
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Superko, Colleen
REGISTRATION INFORMATION:
REFERENCE/DOCKET NUMBER: 106.941.155
TELEPHONE: (617) 526-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02109
COMPUTER READABLE FORM:
                                        HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (9)
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                                                                                                                                       TYPE: amino acids
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STATE: MA
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                                                                                                                  STRANDEDNESS: single
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OF INVENTION: CHARACTERIZATION OF GRANULOCYTIC EHRLICHIA AND METHODS OF USE
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STOREY, James
BELTZ, Gerald A.
                                                                            (genomic)
                                                                                                                                                                                                                        526-5000
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                                                                                                                                                                                                                                                                                 106.941.155
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US-09-328-352-7885
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LENGTH: 1407
TYPE: PRT
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Best Local :
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: GATY L. Breton et al. TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 4.0%; Score 111.5; DB 3; Local Similarity 21.1%; Pred. No. 0.048; hes 95; Conservative 62; Mismatches 178;
                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                           216 LREEIPOTTSETKLKKASKRLKLMEAFKDSNNKPEWMVMNVLPVLPPDLRPLVPLEGGRF 275
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                                                       ATSDLNDLYRRVINRNNRLKRLIDLAAPDIIVRNEKRMLQESVDALLDNGRRGRAITGSN 335
                                                                                                                                                                                                    ESYVVTDPG-WTPFEKYQLLNDEEYFTALEEHGDBFVAKWGAEAVQDLLKDIDLEABISR 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQEVEIVSEGGTQDSLSTNISQDSVGVSTDLEAHSQBVETVSEFTQDSLSTNISQDSVGV 507
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                                                                                                                                                                 -YERFLKTTMTKK---
                                                                                          TT---GQVYEQVL----
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Pred. No. 0.29;
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US-09-252-991A-32742
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32742
LENGTH: 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32742, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                               Matches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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                   AFAEQQPAAIAGEVAEGLDAHRPLAVVEDRHVLAQHRLGGKRQVAIARGRAV----
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                                                            -VGGTVGD
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                        74; Mismatches
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                                                            --IBSLPFLETIROMG----VELGRDRALFIHLTLVP
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PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 21763

LENGTH: 1700

TYPE: DOT
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION UNMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                         Local Similarity
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QGLDDLVVDQLRLDVPAADLSAWEKVVDGLTHPTDEVSIAIVGKYVDHTDAYKSLNEALI 312
                                                              ALAGARHHRVADQPL - -
                                                                                                 LICR----SEQPIPASERRKIALFTNVAEKAVIS----AIDADTIYRIPLLL----RE
                                                                                                                                                                                                                        AVVEVVGR-----RREVVPRAQGADVMQVAAAHQLHVAALDQRTVGCQPTLRLGQVDHRR
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                                                                                                                                                                                                                                                                                                      %; Score 107.5; DB 4;
%; Pred. No. 0.64;
43; Mismatches 158;
                                                              LVETVAEALLASVRVHAQAAEQVVRVEELLQFGERR
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Search comp Job time :	Dp 8	Qy 4	Db 7	Ογ 3	Db 7	<i>Q</i> ;	Db 7
Search completed: January 29, 2004, 15:57:07 Job time : 18.0734 secs	852 GVAGAGDAVVDARAGIDRDVAG 873	422AGELVTRDEDSDLGG 436	792 ARAETEQAVVTLGQAEAGGGNRVDLAFRQVGRQLRGQRHDHRNPAAAHRAVAHLAAAADE 851	WGLEGAHSTEFLPKSPI	734 ALTLDVGRASQAVDSHALALPGTGGVAGALLADRDAATALGAVGAGTERGAAIAVLGE 791	313 HAGIHTRHKVQISYIDSETIEAEGTAKLKNVDAILVPGGFGERGVE-GKIST 363	700 VGLDQVLVAGARR
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Result
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1: /cgn2 6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2 6/ptodata/1/pubpaa/US06 PUBCOMB.pep:*

5: /cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

6: /cgn2 6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

8: /cgn2 6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2 6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

10: /cgn2 6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

11: /cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

12: /cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
   GenCore version (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapext 0.5
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   US-09-815-242-1193

US-09-815-242-11275

US-09-815-242-1175

US-09-815-242-13865

US-09-815-242-13372

US-09-815-242-12378

US-09-815-242-12978

US-09-815-242-10727

US-09-815-242-10727

US-09-815-242-11376

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US-09-934-868-70
US-09-941-947A-16
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(without alignments)
3044.503 Million cell updates/sec
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Compugen Ltd.
Sequence 12, Appl
Sequence 70, Appl
Sequence 16, Appl
Sequence 11933, A
Sequence 10275, A
Sequence 11175, A
Sequence 11375, A
Sequence 12372, A
Sequence 12978, A
Sequence 10727, A
Sequence 10727, A
Sequence 11370, A
Sequence 11310, A
Sequence 14011, A
Sequence 14011, A
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ALIGNMENTS

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                                                                                                                                                                                                         ; OTHER INFORMATION: Amino acid sequences encoded by US-09-934-903-12
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US-09-934-903-12
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
SEQ ID NO 12
LENGTH: 544
                                                                                                                   Query Match
Best Local Similarity
Matches 544; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/09934903
Patent No. US20020102690A1
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Picataggio, Stephen
APPLICANT: Cheng, Qiong
TITLE OF INVENTION: Genes Involved in Isoprenoid Compounds Production
PILE REFERENCE: CL1646 US NA
CURRENT APPLICATION NUMBER: US/09/934,903
CURRENT APPLICATION NUMBER: 60/229,907
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR PILING DATE: September 1, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Koffas, Mattheos
APPLICANT: Odom, J. Martin
APPLICANT: Schenzle, Andrea
APPLICANT: No. US200201026
APPLICANT: Tomb, Jean-Franc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Methylomonas 16a FEATURE:
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Schenzle, Andreas J.
No. US20020102690Alton, I
Tomb, Jean-Francois
Rouviere, Pierre
                                                                  MTXFIFITGGVVSSLGKGIAASSLAAILEDRGLKVTITKLDFYINVDFGTMSFFQHGEVF
  VTEDGAETDLDLGHYERFLKTTWTKKNNFTTGQVYEQVLRNERKGDYLGATVQVIPHITD 120
                                            MTKFIFITGGVVSSLGKGIAASSLAAILEDRGLKVTITKLDPYINVDPGTMSPFQHGEVF
                                                                                                                       100.0%; Score 2788; DB 10; ilarity 100.0%; Pred. No. 1.5e-254; Conservative 0; Mismatches 0; 1
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                                                                                                                                                 Best Local Similarity Matches 544; Conserv
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                                                                                                                                                                                                                         OTHER INFORMATION: Amino acid sequences encoded by ORF6 -
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EIKRRVYESAEGKDVALIEVGGTVGDIESLPFLETIRQMGVELGRDRALFIHLTLVPYIK 180
                                                      VTEDGAETDLDLGHYERFLKTIWTKKNNFTTGQVYEQVLRNERKGDYLGATVQVIPHITD 120
                                                                                       MTKFIFITGGVVSSLGKGIAASSLAAILEDRGLKVTITKLDPYINVDPGTMSPFQHGEVF 60
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                                                                                                                                               100.0%; Score 2788; DB 10; llarity 100.0%; Pred. No. 1.5e-254; Conservative 0; Mismatches 0;
                                                                                                                                                 Indels
                                                                                                                                                                            Length 544;
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Publication No. US20030003528A1
GENERAL INFORMATION:
APPLICANT: Brzostowicz, Patricia C.
APPLICANT: Cheng, Qiong
APPLICANT: Dicosimo, Deana J.
APPLICANT: Koffas, Mattheos
APPLICANT: Miller, Edward S. Jr.
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US-09-941-947A-16
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                                                                                                                                    Matches
                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                        SEQ ID NO 16
                                                                                                                                                                                                                                                                                              APPLICANT: Koffas, Mattheos

APPLICANT: Miller, Edward S. Jr.

APPLICANT: Miller, Edward S. Jr.

APPLICANT: Picataggio, Steve

APPLICANT: Picataggio, Steve

APPLICANT: ROUViere, Pierre E.

TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE

FILE REFERENCE: CL1903 US NA

CURRENT APPLICATION NUMBER: US/09/941,947A

CURRENT APPLICATION NUMBER: 60/229,907

PRIOR APPLICATION NUMBER: 60/229,858

PRIOR PILING DATE: 2000-09-01

PRIOR PILING DATE: 2000-09-01

PRIOR PILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 60
SOFTWARE: Microsoft Office
                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                           ORGANISM: Methylomonas
                                                                                                                                                                                                                                           ENGTH:
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                                                                                                                                    Conservative
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100.0%; F
ative 0;
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                                                                                                                                  Score 2788; DB 11;
Pred. No. 1.5e-254;
Mismatches 0;
                                                                                                                                                                  DB 11;
                                                                                                                                     Indels
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RESULT 4
US-09-815-242-11933
; Sequence 11933, Application
; Sequence 11933, Application
Common No. US20020061569A1
; TYPE: PRT ; ORGANISM: Pseudomonas US-09-815-242-11933
                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR FILING DATE: 2001-10-216
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PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2001-02-6
PRIOR FILING DATE: 2001-02-6
PRIOR FILING DATE: 2001-02-16
NUMBER: 00 SEQ ID NOS: 14110
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T
APPLICANT: Xu, H. Howard
                                                                      SOFTWARE: FastSEQ
SEQ ID NO 11933
LENGTH: 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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Trawial
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             CURRENT APPLICATION NUMBER: US/09/815,24
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
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Best Local (
                                                                                                                                                                                                                                                                                                          APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA, 011A
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Zyskind, Judith W.
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NUMBER: 60/269,308
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US-09-815-242-11175
; Sequence 11175, Application
; Patent No. US20020061569A1
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FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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SOFTWARE: FastSEQ for
SEQ ID NO 10275
LENGTH: 545
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PELLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PELLING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 11175
LENGTH: 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TIYRIPLLLREQGLDDLVVDQLRLDVPAADLSAWBKVVDGLTHPTDBVSIAIVGKYVDHT
                                                          KAGLKVTGLSADKKLVEIIEVENHPWFVACQFHPEFTSTPRDGHPLFAGFVKAAYENHK
               AAGMKPSGKSLDGRLVEIIELPEHPWFLACQFHPEFTSTPRNGHALFSGFVEAA-AKHK 539
                                                                                                                            RTAQYARENKIPYLGICLGMQIALIEYARNVAGLTKANSSEFDKDCEQPVVALITEWQDA
                                                                                                                                              STVRFARENKIPYLGICLGMQSAVIEFARNVVGLEGAHSTEFLFKSPHPVIGLITEMMDE
                                                                                                                                                                                            DAYKSVNBALKHAGLTNRLSVNIKYIDSQDVBTKGVBVLKGIDGILVPGGFGYRGVEGKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNYIFVTGGVVSSLGXGIAAASLAAILEARGLNVTIMKLDPYINVDFGTWSPTQHGEVFV
                                                                                                                                                                                                                                                                                                                   AGEVKTKPTQHSVKELLSIGIQPDVLICRSDRMIPPNERAKIALFCNVAERAVISLKDVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.5%; Score 1908.5; DB 9; 67.5%; Pred. No. 2.2e-171; ive 71; Mismatches 103;
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US-09-815-242-13865
(Sequence 13865, Application US/09815242)
(Sequence 13865, Application US/09815242)
(Patent NO. US20020061569A1)
(GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Prokaryotes
TITIE OF INVENTION: Identification of Essential Genes
TITIE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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CURRENT APPLICATION NUMBER: US/09/815,24:
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION MUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-12-16
PRIOR PILING DATE: 2001-12-16
PRIOR PILING DATE: 2001-12-16
PRIOR PILING DATE: 2001-12-16
PRIOR PILING DATE: 2001-12-16
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PRIOR PILING DATE: 2001-12-16
PRIOR PILING DATE: 2001-12-16
PRIOR PILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-
; Sequence 12372, Application US/09815242
; Patent No. US20020061569A1
                                              RESULT 8
US-09-815-242-12372
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Best Local Similarity
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OTHER INFORMATION: Xaa = -09-815-242-13865
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ORGANISM: Salmonella typhi
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                                                                                                                                                                                                                                                                                AGELVTRDEDSDLGGTMRLGAQKCRLKADSLAFQLYQKDVITERHRHRYEFNNQYLKQLE
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67.4%; Pred. No. 1.5e-159;
ative 64; Mismatches 101;
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Best Local S
Matches 302
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APPLICANT:
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APPLICANT: Haselbeck,
APPLICANT: Ohlsen, Ka
APPLICANT: Zyskind,
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302; Conserv
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILLING DATE: 2000-05-26
PRIOR PILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12372
LENGTH: 536
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification
TITLE OF INVENTION: Prokaryotes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIKFIFVTGGVVSSLGKGITASSLGRLLKDRGLNVTIQKFDPYLNVDPGTMSPYQHGEVF
                                                                                                                                                                            SEGKISAIKYARENNVPFFGICLGWOLATVEFSRNVLGLEGAHSAELDPATPYPIIDLLP 420
                                                                                                                                                                                                           VEGKISTVRFARENKIPYLGICLGMQSAVIBFARNVVGLEGAHSTBFLFKSPHPVIGLIT 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DADTIYRIPLLLREQGLDDLVVDQLRLDVP-AADLSAWEXVVDGLTHPTDEVSIAIVGKY 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UTDDGAETDLDLGHYERFIDINLNKFSNVTAGKVYSHVLKKERRGDYLGGTVQVIPHITN
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LXQLEAAGMKPSGKSLDGRLVEIIELPEHPWFLACQFHPEFTSTPRNGHALFSGFVEAAA 536
                                                                                                          EWMDEAGELVTRDEDSDLGGTMRLGAQKCRLKADSLAFQLYQKDVITERHRHRYBENNQY 476
                                                                                                                                                                                                                                                                                                                                                 VDHTDAYKSLNBALIHAGIHTRHKVQISYIDSBTIEABGTAK-LKNVDAILVPGGFGERG 356
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Zyskind, Judith W.
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ilarity 55.6%;
Conservative 93
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                                                           IBDLGGTLRLGLYPCSIKEGTLAQDVYGKAEIEERHRHRYEFNNDY 470
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Mismatches 13
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RESULT 9
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12978
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Patent No. US20020061569A1
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Best Local (
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITEA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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TYPE: PRT
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)2; Conservative
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                                                                                                                                                       EIKERLLLAGESTNADVVITEIGGTTGDIESLPFIEAIRQIRSDLGRENVMYVHCTLLPY
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 VDHTDAYKSLNEALIHAGIHTRHKVQISYIDSETIEABGTAK-LKNVDAILVPGGFGERG
                               DADSLYEIPLQLSQQNMDDIVIKRLQLNAKYETQLDEWKQLLDIVNNLDGKITIGLVGKY
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Xu, H. Howard
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Best Local Similarity
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Enterococcus faecalis
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Trawick, John D.
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Zyskind, Judith W.
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NUMBER OF SEQ ID NOS: 14110
SOPTWARE: PastSEQ for Windows Version
SEQ ID NO 4984
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APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITER.011A
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
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APPLICATION NUMBER: 60/269,308
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FILING DATE: 2000-11-27
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EIKRRVYESAE--GKDVALIEVGGTVGDIESLPFLETIRQMGVELGRDRALFIHLTLVPY 178
                                                                                                                                                                  MTKYIFVTGGVVSSIGKGIVAASLGRLLKNRGLKVTIQKEDPYINVDPGTMSPYQHGEVP
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                                                     VTDDGAETDLDLGHYERFIDINLNKYSNVTTGKIYSEVLRKERKGEYLGATVQVIPHITN
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                                                                      PRIOR FILING DATE:
NUMBER OF SEQ ID NO.
SOFTWARE: FastSEQ fo
SEQ ID NO 10727
LENGTH: 536
Query Match
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APPLICANT:
APPLICANT:
                             ORGANISM: Enterococcus -09-815-242-10727
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CURRENT APPLICATION NUMBER: US/09/815
CURRENT FILING DATE: 2001-03-21
CURRENT FILING DATE: 2001-03-21
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TITLE OF INVENTION: Identification of
TITLE OF INVENTION: Prokaryotes
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APPLICANT: Ohlsen, K
APPLICANT: Zyskind,
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APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
                                                                                                                                                                              FILING DATE: 2000-10-25
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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FILING DATE: 2000-05-26
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Zyskind, Judith W.
Wall, Daniel
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                                                                                                       ID NOS: 14110
SEQ for Windows Version
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    Score 1569;
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   Length 536;
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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REPERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/219.078
PRIOR APPLICATION NUMBER: 60/206,849
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith
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Zyskind, Judith W.
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Xu, H. Howard
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NUMBER: 60/257,931
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Sequence 11320, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Mail, Daniel
APPLICANT: Tranick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 13376
LENGTH: 535
TWEE: 1855
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ORGANISM: Streptococcus
-09-815-242-13376
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Vanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Esse
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA, 011A
CURRENT APPLICATION NUMBER: US/09/815,242
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Pred. No. 1.6e-138;
B; Mismatches 125;
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; ORGANISM: Helicobacter pylori
US-09-815-242-11320
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-12-22
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SEQ ID NO 11320
LENGTH: 538
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Best Local S
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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PRIOR APPLICATION NUM
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APPLICATION NUMBER: 60/191,078
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                             AGMKPSGKSLDGRIVEIIELPEHPWFLACQFHPEFTSTPRNGHALFSGFVEAA
                                                               HQKQVRTYNSPLGGTMRLGEYECEIMPNSLLEKAYKKPSIKERHRHRYEINPKYRQEWEN
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                                                                                             GELVTRDEDSDLGGTMRLGAQKCRLKADSLAFQLYQKDVITERHRHRYEFNNQYLKQLEA
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RESULT 14
US-10-156-761-14031
US-10-166-761
Sequence 14031, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:

APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:

: CMURA, SATOSHI : IKEDA, HARUO : ISHIKAWA, JUN : HORIKAWA, HIROSHI

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PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14031
LENGTH: 549
Type: nem
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US-09-738-626-5066
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                                                                                  Sequence 5066, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
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APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
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APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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Similarity 52.5%; Pred. No. 2.3e-126;
87; Conservative 92; Mismatches 153; Indels
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                                                                                                                                                                                                       AAVERKT
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SEQ ID NO 5066

LENGTH: 554

TYPE: PRT

ORGANISM: Corynebacterium glutamicum

US-09-738-626-5066
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APPLICANT: TATELSHI, NAOKO
APPLICANT: SENGH, AKHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL: POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-06-03
NUMBER OF SEQ ID NOS: 7059
COFTUNDE: DETOTION OF 30
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Matches 283
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                                                                                                                                                         TKFIFITGGVVSSLGKGIAASSLAAILEDRGLKVTITKLDPYINVDPGTMSPPQHGEVFV
LVKTA 547
                                 FVEAA 535
                                                                   NAYRAQIAEGSDLVFSGTSPDGHLVEFVEYPKEVHPYLVATQAHPEYKSRPTHAHPLFYG
                                                                                                                                        TMEE ---
                                                                                                                                                                                                                                ERGVEGKISTVRFARENKIPYLGICLGMQSAVIEFARNVVGLEGAHSTBFLFXSPHFVIG 413
                                                                                                                                                                                                                                                                                 KYIDLPDAYLSVVBAVRAAGYANWTRTNİKWİTSDDCETPSGAMKALSGLDAİVVPGGFG
                                                                                                                                                                                                                                                                                                                                                  SCPDSSSIYNIPDVLYREHLDTFIIRRLGLPFRDVDWSTWHDLLERVNNPRHELTVGIVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       VPYIKSAGELKTKPTQHSVKELRTIGIQPDILICRSEQPIPASERRKIALFTNVAEKAVI 235
                                                                                         NOYLKOL-EAAGMKFSGKSLDGRLVEIIELPE--HPWFLACOFHPEFTSTPRNGHALFSG
                                                                                                                                                                                                                                                                                                   KYVDHTDAYKSLNEALIHAGIHTRHKVQISYIDSETIEAEGTA--KLKNVDAILVPGGFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEDGAETDLDLGHYERFLDRNLGLNANVTTGKVYSTVIAKERRGEYLGKTVQVIPHITDE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEDGAETDLDLGHYERFLKTTMTKKKNNFTTGQVYEQVLRNERKGDYLGATVQVIPHITDE 121
                                                                                                                                                                                                             IRGIEGKIGAITFAREHKIPLIGICIGLOCTVIBAARO-AGLEOASSTEFDFAATOFVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IKARILSMGEPDAHGNAPDVVISBVGGTVGDIESOPFLRAAROVRHEIGRENCFFIHCSL 189
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                                                                                                                                        - QKAAVSGEADLGGTMRLGAYPATLEEGSLVAELYGTTEVSERHRHRYEVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.2%; Score 1372; DB 10; 51.9%; Pred. No. 1.3e-120; tive 78; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78;
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969

Search completed: January 29, Job time: 38.1346 secs

2004,

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Perfect score:
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Result No.

Database

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1355.5	1356	1356.5	1362	1365.5	1369.5	1374.5	1423	1434	1441.5	1444.5	1449	1484	1507	1538.5	1542
48.6	48.6	48.7	48.9	49.0	49.1	49.3	51.0	51.4	51.7	51.8	52.0	53.2	54.1	55.2	55.3
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D86520	D90161	A72103	B84334	B70503	C71342	D69281	B75379	C86686	T36879	E64563	C71946	E69154	F81418	H71189	S25101
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ALIGNMENTS

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361 ISTVRFARENKIPYLGICLGMQSAVIBFARNVVGLEGAHSTEFLPKSPHPVIGLITEMVD	301 TDAYKSLNEALIHAGIHTRHKVQISYIDSETIEAEGTAKLKNVDAILVPGGFGERGVBGK	241 DTIYRIPLLIREQGLDDLUVDQLRLDVPAADLSAWEKVVDGLTHPTDBVSIAIVGKYVDH	181 SAGELKTKPTQHSVKELRTIGIQPDILICRSBQPIPASERRKIALPTNVAEKAVISAIDA	121 EIKRRVYESABGKDVALIEVGGTVGDIESLPFLETIRQMGVELGRDRALFIHLTLVPYIK :: : :	61 VTEDGAETDLDLGHYERFLKTIMTKKNNFTTGQVYEQVLRNERKGDYLGATVQVIPHITD	1 MTKFIFITGGVVSSLGKGIAASSLAAILEDRGLKVTITKLDFYINVDFGTMSFFQHGEVF :: :	72.0%; Score 2008; DB 2; Similarity 71.2%; Pred. No. 3.1e-121; 3; Conservative 64; Mismatches 91;	CTP synthase PA3637 [imported] - Pseudomonas aeruginosa (strain PAOI) C;Species: Pseudomonas aeruginosa C;Bate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: B83192 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.: Bri adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.: Lim, ; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathox A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Recession: B83192 A;Status: preliminary A;Recession: preliminary A;Residues: 1-542 <sto> A;Recession: 1-542 <sto> A;Experimental source: Strain PA01 C;Genetics: A;Gene: pyrG; PA3637 C;Superfamily: CTP synthase</sto></sto>	
SELPKSPHPVIGLITEWMD 420	WDAILVPGGFGERGVBGK 360	ITHPTDEVSIAIVGKYVDH 300 	(IALFINVAEKAVISAIDA 240 : : (IALFINVEERAVIALEDV 240	ELGRDRALFIHLTLVÞYIK 160 -	ERKGDYLGATVQVIPHITD 120 - ERGDYLGATVQVIPHITD 120	ALINADEGLASPEOHOBAE 60	Length 542; Indels 0; Gaps 0;	<pre>(strain PAO1) c_change 31-Dec-2000 c_change 31-Dec-2000 c, K.R.; Kas, A.; Larbig, K.; Lim, t nosa PAO1, an opportunistic pathog 3 786; PIDN:AAG07025.1; GSPDB:GN0012</pre>	

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A; Residues: 1-545 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;

A;Title: Complete genome sequence of a multiple drug resistant

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AD0859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Parkhill, J.; Dougan, G.; van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTP synthetase (imported) - Salmonella enterica subsp. enterica serovar Typ C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AD0859
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Best Local
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                                                                                      AGELVIRDEDSDLGGTMRLGAQKCRLKADSLAFQLYQKDVITERHRHYBFNNQYLKQLE 481
                                                                                                                                                                                                                                                                                     TIYRIPLLLREQGLDDLVVDQLRLDVPAADLSAWEKVVDGLTHPTDBVSIAIVGKYVDHT 301
                                                                                                                                                                                                                                                                                                                 AGEVKTKPTQHSVKELLSIGIQPDILICKSDRAVPANERAKIALFCNVPBKAVISMKDVD
                                                                                                                                                                                                                                                                                                                                                                              KERVLEGGEGHDVVLVEIGGTVGDIESLPFLEAIRQLAVDIGREHALFMHUTLVFYLAA 182
                                                                                                                                                                                                                                                                                                                                                                                                      IKRRVYESAEGKDVALIEVGGTVGDIESLPFLETIROMGVELGRDRALFIHLTLVPYIKS
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                            AAGMKFSGKSLDGRLVEIIELPEHPWFLACQFHPEFTSTPRNGHALFSGFVEAAAKHK 539
                                                                                                                             ATARYAREMNIPYLGICLGMQVALIEFARNVAGMDNANSTEFVPDCKYPVVALITEWRDE 422
                                                                                                                                             STVRFARENKIPYLGICLGMQSAVIEFARNVVGLEGAHSTEFLPKSPHPVIGLITEWMDE 421
                                                                                                                                                                                         DAYKSVIEALKHGGLKNRVTVNIKLIDSQDVETRGVEILKDLDAILIPGGPGYRGVEGKI
                                                                                                                                                                                                                      DAYKSLNEALIHAGIHTRHKVQISYIDSETIBAEGTAKLKNVDAILVPGGFGERGVEGKI 361
                                                                                                                                                                                                                                                    SIYKIPGLLKSQGLDDYICKRFSLNCPEANLSEWEQVIYEEANPAGEVTIGMVGKYIELP
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AAGLRVAGRSGDDQLVEIIEVPNHPWFVACQFHPBFTSTPRDGHPLFAGFVKAANEHQ
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68.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73;
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Pred. No. 3e-117
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 SYECTP
SYNTHASE (EC 6.3.4.2) [validated] - Escherichia coli (strain K-12)
N;Alternate names: CTP-synthetase; UTP-ammonia ligase
C;Species: Escherichia coli
C;Species: 1-Mar-1988 #sequence_revision 21-Nov-1997 #text_change 01-Mar-2002
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A;Gene: VC2448
A;Map position:
C;Superfamily: (
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B82074

E82074

CTP synthase VC2448 [imported] - Vibrio cholerae (strain N16961 serogroup C;Spectes: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-200
C;Accession: E82074
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A;Residues: 1-545 (HEI>
A;Cross-references: GB:AE004315; GB:AE003852; NID:g9657024; PIDN:AAF95590.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
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Nature 406, 477-483, 2000
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                                     AAGMKFSGKSLDGRLVEIIELPEHPWFLACOPHPEFTSTPRNGHALFSGFVEAAAK 537
                                                                                                                   AGELVTRDEDSDIGGTWRLGAQKCRLKADSLAFQLYQKDVITERHRHRYEFNNQYLKQLE
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KAGLKVSGLSADKKLVEVIENPAHPWPVAAQPHPBPTSTPRDGHPLFAGFVKAAGQ
                                                                              EGNVEERSEKSDLGGTMRLGSQLCHLEKGTKAYELYGSATIHERHRHRYEVNNLLRPQIE
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Pred. No. 7.7e-116;
6; Mismatches 98;
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A; Title: Nucleotide sequence of Escherichia coli pyrG encoding
A; Reference number: A92584; MUID:86168304; PMID:3514618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H65959
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A;Residues: 1-337,'L',339-475,'S',477-488,'RA',491-545
A;Cross-references: GB:M12843
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                                                                                 AAGMKFSGKSLDGRLVEIIELPEHPWFLACQFHPEFTSTPRNGHALFSGFVEAAAK 537
                                                                                                                                                    AGELVTRDEDSDIGGTMRIGAQKCRIKADSIAFQIYQKDVITERHRHRYBFNNQYIKQIB
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67.7%;
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Pred. No. 2.5e-115;
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A;Title: Genome sequence of enterohemorrhagic Escherichia coli
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85929
A;Status: preliminary
A;Molecule type: DNA
                                                                               A85929

CTP synthetase [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli
C;Pate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_chang
C;Accession: A85929
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner
Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.
Nature 409, 529-533, 2001
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Escherichia

COLL

(strain O157:H7, substrain RIMD 0509952)

16-Feb-2001 #text_change

substrain

EDL933)

14-Sep-2001 J.D.; Rose, Potamousis,

A.; Dimalanta, E.;

D.J.;

O157:H7

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C;Species: Escherichia coli
C;Date: 18-Uul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: H91083
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; H
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H91083
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C;Superfamily: (
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
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A; Residues: 1-545 < HAY >
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DAGLRVAGRSGDDQLVEIIEVPNHPWFVACQFHPBFTSTPRDGHPLFAGFVKAASE
                          AAGMKFSGKSLDGRLVEIIELPEHPWFLACQFHPKFTSTPRNGHALFSGFVEAAAK 537
                                                                                                                     AGELVTRDEDSDLGGTMRLGAQKCRLKADSLAFQLYQKDVITERHRHRYEFNNQYLKQL3
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                                                                                        NGNVEVRSEKSDLGGIMRLGAQQCQLVDDSLVRQLYNAPTI VERHRHRYBVNNMLLKQI B
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Pred. No. 2.5e-115;
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A;Status: preliminary
A,Molecule type: DNA
A,Holecule type: DNA
A,Presidues: 1-545 < KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92607.1; PID:g15981303; GSPDB:GN00175
C;GenetLos:
A;Gree: pyrG
C;Superfamily: CTP synthase
C;Keywords: ligase
                                                                                                                                                                                                                                            CTP synthase (EC 6.3.4.2) [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Accession: AC0410
C;Accession: AC0410
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, R;Parkhill, J; Wren, B.W.; Thomson, T. Cronin, A.; Davies, R.M.; Davis, P.; Dougan, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: pyrG
C;Superfamily: CTP synthase
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A;Cross-references: GB:AE005174; NID:g12517252; PIDN:AAG57893.1; GSPDB:GN00145; UWGP:Z40
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
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Matches 363
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Score 1909; DB 2;
Pred. No. 7.1e-115;
O; Mismatches 102;
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Pred. No. 2.5e-115;
1; Mismatches 102;
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AAGMKPSGKSLDGRLVEIIELPEHPWELACQFHPEFTSTPRNGHALFSGFVEAAAKHK 539
                                                                                                   AGELVIRDEDSDLGGTMRLGAQKCRLKADSLAFQLYQKDVITERHRHRYBFNNQYLKQLE
                                                                                                                                             LAARYAREHNIPYLGICLGMQVALMEFARNVAGMENANSTEFVPDCKYPVVALITEWRDE
                                                                                                                                                                         STVRFARENKIPYLGICLGMQSAVIEFARNVVGLEGAHSTEFLFKSPHPVIGLITEMMDE
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                                                                                                                                                                                                                                                  DAYKSLNEALIHAGIHTRHKVQISYIDSETIEAEGTAKLKOVDAILVPGGFGERGVEGKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TEDGAETDLDLGHYERFIRTKMTRRNNFTTGRIYSEVLRKERRGDYLGATIQVIPHITMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEDGAETDLDLGHYERFLKITMIKKNNFITGQVYEQVLRNERKGDYLGATVQVIPHITDE 121
                                                                      DGNVEIRTEESDLGGTMRVGGQQCHLTEGSLVRQMYGEPTIVERHRHRYEVNNMLLKQIE
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CTP synthase (BC 6.3.4.2) - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Jate: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 16-Jul-1999
C;Accession: F64181
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, B.F.; Kerlavage, J. Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, Gocayne, J. Scott, J.; Shirley, R.; Liu, Fuhrmann, J.L.; Geoghagen, N.S.M., D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Aecession: F64181 A;Cross-references: GB:U32788; GB:L42023; NID:g1574629; C;Superfamily: CTP synthase C;Keywords: ligase; pyrimidine nucleotide biosynthesis A; Molecule type: DNA A; Residues: 1-545 < TIGR> A;Status: nucleic acid sequence not shown; translation not shown Matches Query Match Best Local 9 122 364; 63 62 w Similarity IKRRVYESAEGKDVALIEVGGTVGDIESLPFLETIRQMGVELGRDRALFIHLTLVPYIKS Conservative 68.5%; Score 1908.5; DB 2; 67.5%; Pred. No. 7.6e-115; 71; Mismatches 103; Length PIDN:AAC22733.1; PID:g1574630; 1; Gaps 181 122 121 62 61 <u>,,</u> **C** 5

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submitted to GenBank, June 2000

A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Kttajima, J.P.; Krieger, J.B.; Kuramae, E.B.; Laigu J.D.; Jungueira, M.L.; Kemper, S.L.; Kttajima, J.P.; Krieger, J.B.; Kuramae, E.B.; Laigu Chado, M.A.; Madeira, A.M.; Marcino, C.L.; Marques, M.V.; Martins, E.A.; Aluthors: Martins, E.M.F.; Madeira, A.Y.; Menck, C.F.M.; Miracca, B.C.; Miyaki, C.Y.; P.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.F.; P.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, A.C.R.; Ga Silvai, J.V.; Varjovski-Almeida, S.; Vettore, A.L.; A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 bel A;Accession: C82700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTP synthetase XF1288 (imported) - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Date: 18-Aug-2000
C;Accession: C82700
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide
Nature 406, 151-157, 2000
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C; Genetics:
A; Gene: XF1288
C; Superfamily: CTP syn1
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer,
Briones, D. Docena, C. Docena, C. Docena, C. Camargo, A. P.; Ferreira, A.J.S.
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                              VTBDGAETDLDLGHYERFLKTTMTKKNNFTTGQVYEQVLRNERKGDYLGATVQVIPHITD 120
                                                                                                                 MTXFIFITGGVVSSLGKGIAASSLAAILEDRGLKVTITKLDPYINVDPGTMSPFQHGEVF
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  VTDDGAETDLDLGHYERFVRTRLSRNNSVTTGRIYQNVICKERRGDYLGATVQVIPHITD
                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                               synthase
                                                                                                                                                                       68.3%; Score 1905; DB 2; 66.1%; Pred. No. 1.3e-114; ative 79; Mismatches 102;
                                                                                                                                                                                                                   Length 554;
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C;Superf
C;Keywor
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: P81798
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-544 <PAR>
A;Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB84970.1; PID:g7380384
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTP synthase (BC 6.3.4.2) NMA1742 [imported] - Neisseria meningitidis (strain C;Species: Neisseria meningitidis C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C;Accession: F81798
C;Accession: F81798
C;Accession: F81798
C;Accession: Manageris K.J. James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S; Hollroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; R Hature 404, 502-506, 2000
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Best Local
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Superfamily: CTP synthase
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                                                                                                                                                                                                                                                                                                         67.9%; Score 1892.5; DB 2 66.1%; Pred. No. 8.1e-114; Live 80; Mismatches 101;
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RTTTGEVERRDEKSDLGGTMRLGLQEQRLKAGTLVRELYGRDVVGERHRHRYEFNNRYRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGELKTRPTQHSVKELRSIGIQPDVLLCRSEQVIPDSERRKIALPTNVSERAVIGCPDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDEAGELVTRDEDSDIGGTMRLGAQKCRLKADSLAFQLYQKDVITERHRHRYEFNNQYLK 478
                                                                                                                                                                                                                                                                                      GKVLASRYARBQRVÞYFGICYGMQAAVVDYARHVAGLEGANSTENDRQSPHPVIALITEW
                                                                                                                                                                                                                                                                                                                                                                                                                                       DYQDAYKSVGEALKHGGLRQRTKVNLKWVEAQDLEGSDMGALKDIDGILVPGGFGDRGFE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DHTDAYKSLNEALIHAGIHTRHKYQISYIDSETIEAEGTAKLKNYDAILVPGGFGERGVE 358
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QLEDAGLVIAAKSMDDTLVEMIELPREMHPWFLACQAHPEFLSTPRDGHPLFIGFVKAAR 540
                                                                    QUBAAGMKFSGKSLDGRIVEIIELPE--HPWFLACQFHPEFTSTPRNGHALFSGFVEAAA 536
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WTKFIFITGGVVSSLGKGIAASSLAAILEDRGLKVTITKLDPYINVDPGTMSPFQHGEVF EIKRRVYBSAEGKDVALIEVGGTVGDIESLPFLETIROMGVELGRDRALFIHLTLVPYIK 180 VTEDGAETDLDLGHYERFLKTTMTKKNNFTTGQVYEQVLRNERKGDYLGATVQVIPHITD 120 SAGELKTKPTQHSVKELRTIGIQPDILICRSEQPIPASERRKIALFTNVAEKAVISAIDA BIKRRIHEGAAGYDVAIVEIGGTVGDIESLPFLEAIRQMRSQLGRUNTLFAHLSYVPYIA 180 VTDDGABTDLDLGHYERFIDSTMTRRNSFSTGQVYENVIAKERRGDYLGGTVQVIPHITD 120 60

S B S ğ 8

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R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, i. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Pleischmann, R.D.; Dougherty, B., ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A;Authbors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58: A;Reference number: A81000; MUID:20175755; PMID:10710307

A;Accession: F81070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTP synthase NMB1554 [imported] - Neisseria meningitidis (strain MC58 serogroup C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C;Accession: F81070
                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: NMB1554
C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-544 <TET>
A; Cross-references: GB:AE002505;
A; Experimental source: serogroup
C; Genetics:
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Best Local S
Matches 359
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                                                  QTADGSVETRDESADLGGTMRLGAQEVELKAGSLAAKIYGSEHIRERHRHRYEVNNYYYP 480
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                                                                                                                                                             EIKRRVYESAEGKDVALIEVGGTVGDIESLPFLETIRQMGVELGRDRALFIHLTLVPYIK 180
                                                                                                                                                                                                                                                                       MTKFIPVTGGVVSSLGKGIAAASIAAILESRGLNVIMLKLDPXINVDPGTMSPPQHGEVF
                                                                                                                                                                                                                                                                                                        MTKFIFITGGVVSSLGKGIAASSLAAILEDRGLKVTITKLDPYINVDPGTMSPFQHGEVF
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DTIYRIPLLLREQGLDDLVVDQLRLDVPAADLSAWBKVVDGLTHPTDEVSIAIVGKYVDH 300
                                                                                                                                                                                                VTDDGAETDLDLGHYERFIDSTWTRRNSFSTGQVYENVIAKERRGDYLGGTVQVIPHITD
                                                                                                                                                                                                                       VTEDGAETDLDLGHYERFLKTTWTKKNNFTTGQVYEQVLRNERKGDYLGATVQVIPHITD
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B, strain MC58
                                                                                                                                                                                                                                                                                                                                            Score 1888.5; DB 2
Pred. No. 1.5e-113;
7; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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C;Superfamily: CTP |
C;Keywords: ligase
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A;Experimental source: strain APS
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A;Molecule type: DNA
A;Residues: 1-545 <STO>
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A;Title: Genome sequence of the endocellular bacterial symbiont o A;Reference number: A34930; MUID:20445173; PMID:10993077
A;Accession: B84978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B84978
CTP synthase (EC 6.3.4.2) [imported] - Buchnera sp.
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Best Local
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Similarity 61.4%;
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                                  NAIKERIILGSENSNIILVEIGGTVGDIESLPFLEAIRQMAVDIGRKNVIYIHLTLVPYI
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                                                                                                                                            ADTIYRIPLLEREQGEDDLVVDQLREDVPAADESAWEKVVDGLTHPTDEVSIAIVGKYVD
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   KISTVRFARENKIPYLGICLGMQSAVIBFARNVVGLEGAHSTEFLPKSPHPVIGLITEWM
                                                                       HTDAYKSLNEALIHAGIHTRHKVQISYIDSETIEAEGTAKLKNVDAILVPGGFGERGVEG
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; Pred. No. 7.7e-104; 
90; Mismatches 117;
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A;Cross-references: GB:AP001520; GB:BA0000004; NID:g10176401; PIDN:BAB07511.1; A;Experimental source: strain C-125 C;Genetics:
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CTP synthetase ctrA (imported) - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence_revision 0i-Dec-2000 #text_change 15-Jun-2001

C;Accession: H84123

R;Takami, H, Nakasone, K, Takaki, Y, Maeno, G, Sasaki, R, Masui, N, Fuji, F, Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans

A;Reference number: A83650; MUID:20512582; PMID:11058132
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Best Local Similarity
Matches 311; Conserv
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                                                                                      GKI EAIRYAREQKI PELGICLGMQLASIEFARNVLGLEGAHSAEINPDTPHPIIDLLPEQ
                                                                                                         GKISTVRFARENKIPYLGICLGMQSAVIEFARNVVGLEGAHSTEFLFKSPHPVIGLITEW
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                                                        MDEAGELVTRDEDSDLGGTMRLGAQKCRLKADSLAFQLYQKDVITZRHRHRYBFNNQYLK
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                            EDMGGTLRLGLYPCKLKNGTLAQSAYNDQVIYERHRHRYEFNNQYRE
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C;Superf
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CTP synthetase - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 16-Jul-1999
C;Accession: F70415
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Gral
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A; Title: Th
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468 480 415 420 300

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PID:g2983754; GB:AE000657

Aquifex

aeolicus.

A.L.; Graham,

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DADTIYRIPLLLREQGLDDLVVDQLRLDVPAADLSAWEKVVDGLTHPTDEVSIAIVGKYV 298	Qy 239 DADTIYRIPLLLREQGLDDLVVDQLR : :: DADNLYSIPLELQKQGLDKLVCEHMK
IKSAGELKTKPTQHSVKELRTIGIQPDILICRSEQPIPASERRKIALFTNVAEKAVISAI 238	Qy 179 IKSAGELKTKPTQHSVKELRTIGIQE :
EIKRRVYESABGKDVALIEVGGTVGDIESLPFLETIRQMGVELGRDRALFIHLTLVPY 178	Qy 121 EIKRRVYESAEGKDVALIEVGGTV : : : : Db 121 ELKDRVYRAGKETNADVVITEIGGTV
VTEDGAETDLDLGHYERFLKTTMTKKNNFTTGOVYEQYLRNERKGDYLGATVQVIFHITD 120 : :	Qy 61 VTEDGAETDLDLGHYERFLKTTMTKK
MTKFIFITGGVVSSLGKGIAASSLAAILEDRGLKVTITKLDPYINVDPGTMSPFQHGEVF 60	Qy 1 MTKFIFITGGVVSSLGKGIAASSLAA : : : Db 1 MTKYIFVTGGVVSSLGKGIVAASLGR
Score 1622.5; DB 1; Length 535; Pred. No. 1.7e-96; 94; Mismatches 127; Indels 13; Gaps 3;	3.2%; 7.0%; 7e 94
nin Nynthase Dyrimidine nucleotide biosynthesis	Gene: ctrA; pyrG Gene: ctrA; pyrG Map position: 37 m Superfamily: CTP s Keywords: ligase;
BH:ALO09126; NID:g2636240; PIDN:CAB15743.1; PID:g2636252 58 camine amidotransferase that catalyzes the terminal react	A; Cross-references: GB:Z99123; GB:AL0091 A; Experimental source: strain 168 C; Comment: This enzyme is a glutamine am
not shown; translation not shown	A; Status: nucleic acid sequence not show A; Molecule type: DNA
Nuence of the Gram-positive bacterium Bacillus subtilis.	A;Title: The complete genome sequence of A;Telerence number: A69580; MUID:9804403 A;Accession: C69610
xa, 1.; letperta, F.; logioni, A.; losato, V.; ochiyama, moto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K stein, E.; Yoshikawa, H.; Danchin, A.	areuchi, M.; Iamaroshi, A.; Iamaro, H.; T.; Winters, P.; Wipat, A.; Yamamoto, H. A;Authors: Yoshikawa, H.F.; Zumstein, E.
Dudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, Ler, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serov	y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B Rieger, M.; Rivolta, C.; Rocha, E.; Roc A; Authors: Schleich, S.; Schroeter, R.;
A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. rogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel	<pre>iech, J.; Harwood, C.R.; Henaut, A.; Hil Koetter, P.; Koningstein, G.; Krogh, S.; A;Authors: Lauber, J.; Lazarevic, V.; Le</pre>
C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler	Nature 390, 249-256, 1997 A;Authors: Foulger, D.; Fritz, C.; Fujit
A;Cross-references: EMBE:249782; NID:g853752; PIDN:CAA89870.1; PID:g853762 R;Kunst, F; Ogasawara, N; Moszer, I.; Albertini, A.M.; Alloni, G; Azevedo, V.; Berter C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Brringron, J.; Pabret, C.; Perrari, R. A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Brringron, J.; Pabret, C.; Perrari, R.	A;Cross-references: EMBE:Z49782; NID:g85 R;Kunst, F; Ogasawara, N.; Moszer, I.; C.; Bron, S.; Brouillet, S.; Bruschi, C. A.; Ehrlich, S.D.; Emmerson, P.T.; Enria
	A;Accession: S55423 A;Molecule type: DNA A;Residues: 1-535 <gla></gla>
ary, May 1995 encing of the Bacillus subtilis chromosomal region from 3	submitted to the EMBL Data Library, May A,Description: Cloning and sequencing of A,Reference number: S55414
NID:g460910; PIDN:AAA16801.1; PID:g143597	A;McCession: A32334 A;Molecule type: DNA A;Residues: 1-535 <tra> A;Cross-references: GB:M22039; NID:g460910; PIDN:AAA16801.1; PID:g1 R;Claser. P.; Danchin. A.</tra>
988 ranscriptional analysis of the spoOF region of the Bacil 9:88314920; PMID:2457578	J. Bacteriol. 170, 4194-4208, 1988 A;Title: Complete sequence and transcrip A;Reference number: A91883; MUID:8831492
evision 30-Jun-1992 #text_change 16-Jun-2000 1610 got, P.; LeCoq, D.; Hoch, J.A.	C;Species: BaCIIIUS SUDCIIIS C;Date: 30-Jun-1992 #sequence revision 3 C;Accession: A32354; S55423; C69610 R;Trach, K.; Chapman, J.W.; Piggot, P.;
se; UTP-ammonia ligase	N/Alternate names: CTP-synthetase; UTP-a

Search completed: January 29, 2004, 15:55:33 Job time: 17.0063 secs

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MEDLINE=22586410; PubMed=12700255;

Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land
Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto
Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;

"Complete genome sequence of the ammonia-oxidizing bacterium a
obligate chemolithoautotroph Nitrosomonas europaea.";
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EMBL; AR061753; AAC33441.1; --
HAMAP; MP 01227; -; 1
InterPro; IPR000991; GATase 1.
InterPro; IPR004468; PyrG.
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TIGRFAMs; TIGRRO0337; PyrG; 1.
PROSITE; PS00442; GATASE TYPE I; 1.
PROSITE; PS00442; GATASE TYPE I; 1.
PROMATINE biosynthesis; Ligase; Glutamine amidotransferase.
Promator romain.
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MEDLINE=98377731; PubMed=9711852;
Mahony T.J., Miller D.J.;
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either L-glutamine or ammonia as the source of nitrogen (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00117; GATase;
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SUBUNIT: Homotetramer (By similarity).
SIMILARITY: Belongs to the CTP synthase family.
SIMILARITY: Contains 1 type-1 glutamine amidotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).

CATALYTIC ACTIVITY: ATP + UTP + NH(3) = ADP + phosphate + CTP.

ENZYME REGULATION: Allosterically activated by GTP, when glutamine is the substrate. Inhibited by CTP (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: Pyrimidine biosynthesis; conversion of
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                                                                                                                TDAYKSLNEALIHAGIHTRHKVQISYIDSETIEAEGTAKLKNVDAILVPGGFGERGVEGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VTEDGAETDLDLGHYERFLKITMTKKNNFTTGQVYBQVLRNERKGDYLGATVQVIPHITD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIKRRVYESAEGKDVALIEVGGTVGDIESLPFLETIRQMGVELGRDRALFIHLTLVPYIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WTKFVFVTGGVVSSLGKGIAAASLAALLETRGIRVTILKLDPYINVDPGTMNPFQHGEVF
ISTVRFARENKIPYLGICLGMQSAVIEFARNVVGLEGAHSTEFLPKSPHPVIGLITEWMD
                                                                          TESYKSLSEALIHAGIHTRCKINIHYIDSENIEQHGTGCLTNMDAILVPGGFGKRGVEGK
                                                                                                                                                                                                                                                                                                                                                                                  SAGELKTKPTQHSVKELREIGIQPDVLLCRSDRPLPLBERRKIALFTNVREBSVISAIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EIKLFIRNGVSDAQVAIVEIGGTVGDIESLPFLEAIRQMSVQLPHHDTCFIHLTLLPYIS
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GLUTAMINE AMIDOTRANSFERASE.
GATASE (BY SIMILARITY).
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GATASE (BY SIMILARITY).
G -> A (IN REF. 2).
E -> D (IN REF. 2).
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MEDLINE=21534947; PubMed=11677668;
Parkhill J. Dougan G. James K.D., Thomson N.R., Pickard D., Wain J.,
Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
Charcher S., Basham D., Brooks K., Chillingworth T., Connerton P.,
Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609; McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latre: Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., L. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvann Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;

MEDLINE=22591367; PubMed=1644504;

Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;

"Comparative genomics of Salmonella enterica serovar Typhi strains
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
CTP synthase (EC 6.3.4.2) (UTP--ammonia ligase)
PYRG OR SYM2953 OR STY3082 OR T2854.
Salmonella typhin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of a multiple
enterica serovar Typhi CT18.";
Mature 413:848-852(2001).
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[2]
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Enterobacteriaceae; Salmonella.
MCBI_TaxID=602, 601;
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                                                                                                                                                                                                                                                                                                                                                                          "Comparative and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              Bacteriol. 185:2330-2337(2003).
- FUNCTION: Catalyzes the ATP-dependent amination either L-glutamine or ammonia as the source of r
                                                                                                                  Similarity).

CATALYTIC ACTIVITY: ATP + UTP + NH(3) = ADP + phosphate + ENCZYME REGULATION: Allosterically activated by GTP, when g is the substrate. Inhibited by CTP (By similarity).

PATHWAY: Pyrimidine biosynthesis; conversion of UMP to CTP
   SUBUNIT: Homotetramer (By similarity).
SIMILARITY: Belongs to the CTP synthas
SIMILARITY: Contains 1 type-1 glutamin
                                                                                                 (last) step.
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glutamine
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         amidotransferase
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S., Layman
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RESULT 4
PYRG_XANCP
ID PYRG_XANCP
AC Q8P9Z6;
DT 28-FEB-2003

STANDARD;

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EMBL; AL627276; CAD06059.1; -.
EMBL; AE016843; AA070411.1; -.
StyGene; SG?????; pyrG.
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InterPro; IPR000991; GATase_1.
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Pyrimidine biosynthesis; Ligase; Glutamine amidotransferase;
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AAGLRVAGRSGDDQLVEIIEVPNHEWEVACQPHPEFTSTPRDGHPLFAGFVKAANEHQ
               AAGMKFSGKSLDGRLVBIIELPEHPWFLACQFHPEFTSTPRNGHALFSGFVEAAAKHK 539
                                              DGIVLEVRSEKSDIGGTWRIGAQQCQLSDGSLVRQLYGASTIVERHRYEVNIWLIKQIE
                                                                 AGELVTRDEDSDIGGTMRIGAQKCRLKADSLAFQLYQKDVITERHRHRYEFNNQYLKQLE
                                                                                                                                               DAYKSVIBALKHGGLKNRVTVNÍKLÍDSQDVETRGVEILKDLDAÍLÍPGGFGYRGVEGKI
                                                                                                                                                                       DAYKSLNEALIHAGIHTRHKVQISYIDSETIEAEGTAKLKNVDAILVPGGFGERGVEGKI
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                                                                                                                                                                                                                                                                                               IKRRVYESAEGKDVALIEVGGTVGDIESLPFLETIRQMGVELGRDRALFIHLTLVPYIKS
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AMIMATOR DOMAIN.
GLUTAMINE AMIDOTRANSFERASE.
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1946;
Pred. No. 1.
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RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., Bl-Dorry H.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., Bl-Dorry H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Setubal J.C., Kitajima J.P.,

"Comparison of the genomes of two Xanthomonas pathogens with differing

It Nature Altices "Comparison"

La Nature Altices "Comparison of the genomes of two Xanthomonas pathogens with differing
                                                                                                                              Query Match
Best Local S
Matches 367
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28-FEB-2003 (Rel. 41, Last annotation update)
CTP synthase (EC 6.3.4.2) (UTP--ammonia ligase)
PYRG OR XCC1697.
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MEDLINE-22022145; PubMed=12034217;
da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
Camarotte G. Carrayan F. Cardon T. Chambergo E. Galina I. D.
                                                                                                                                                                                                                                 DOMAIN
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Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE012271; AAM40991.1; ALT_INIT. HAMAP; MF 01227; -; I. InterPro; IPR000991; GATase 1. InterPro; IPR004468; PyrG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annousentities requires a license agreement (See http://www.isb-sib.ch/annousentities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                            Complete
                                                                                                                                                                                                                                                                                                                                                                                                                  Pyrimidine
                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Homotetramer (By similarity). SIMILARITY: Belongs to the CTP synthase SIMILARITY: Contains 1 type-1 glutamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ure 417.459-463(2002).
FUNCTION: Catalyzes the ATP-dependent amination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          either L-glutamine or ammonia similarity).
CATALYTIC ACTIVITY: ATP + UTP
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367; Conser
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                                                                       MTKFIFITGGVVSSLGKGIAASSLAAILEDRGLKVTITKLDPYINVDPGTMSPPQHGEVF
                              MTPLIFVTGGVVSSLGKGIAAASLASILEARGLKVTYMKLDPYINVDPGTMSPPQHGEVY
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PS00442; GATASB_TYPE_I;
e biosynthesis; Ligase;
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GLUTANINE AMIDOTRANSFERASE.
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
                                                                                                                              80;
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                                                                                                                                 Mismatches

    Glutamine amidotransferase;

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                                                                                                                                                          4e-114;
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Q87LP9;
15-SEP-2003 (Rel
15-SEP-2003 (Rel
15-SEP-2003 (Rel
15-SEP-2003 (Rel
CTP synthase (EC
PYRG OR VP2562.
                                                                                                                                                           Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Ta
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y.,
Yasumaga T., Honda T., Shinagawa H., Hattori K., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic
distinct from that of V. cholerae.";
Lancet 361.743-749(2003).
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=RIMD 2210633 / Serotype 03:
MEDLINE=22508454; PubMed=12620739;
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                             Vibrio parahaemolyticus
                                                                               CATALYTIC ACTIVITY: ATP + UTP + NH(3) = ADP + phosenzyME REGULATION: Allosterically activated by GTI is the substrate. Inhibited by CTP (By similarity)
             SIMILARITY: Belongs to the CTP synthase family.
SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
                                         SUBUNIT:
                                                                                                                                       FUNCTION: Catalyzes the ATP-dependent amination either L-glutamine or ammonia as the source of r
                                                                     PATHWAY:
                                                                                                                           similarity
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3 (Rel. 42, Last s
8e (EC 6.3.4.2) (U
                                       Homotetramer (By similarity).
                                                                   Pyrimidine biosynthesis;
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(UTP--ammonia ligase)
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ACT SITE
ACT SITE
Xanthomonas axonopodis (pv. Bacteria; Proteobacteria; Gaxanthomonadaceae; Xanthomona
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                      -FEB-2003 (Rel. 41, Create
-FEB-2003 (Rel. 41, Last s
-FEB-2003 (Rel. 41, Last a
-FSP) synthase (EC 6.3.4.2) (URG OR XAC1716.
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            Gammaproteobacteria;
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GATASE (BY SIMILARITY).
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RA Camarotte G., Cannavan F., Cardozo J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighteri B.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Moreira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,
RA Setubal J.C., Kitajima J.P.,
ROCEMBARISON of the genomes of two Xanthomonas pathogens with differing the control of the genomes of two Xanthomonas pathogens with differing the control of the genomes of two Xanthomonas pathogens with differing the control of the genomes of two Xanthomonas pathogens with differing the control of the genomes of two Xanthomonas pathogens with differing the control of the genomes of two Xanthomonas pathogens with differing the control of the genomes of two Xanthomonas pathogens with differing the control of the genomes of two Xanthomonas pathogens with differing the control of the genomes of two Xanthomonas pathogens with differing the control of the genomes of two Xanthomonas pathogens with differing the control of the genomes of two Xanthomonas pathogens with differing the control of the genomes of two Xanthomonas pathogens with differing the control of the genomes of two Xanthomonas pathogens with differing the control of the genomes of two Xanthomonas pathogens with differing the control of the genomes of two Xanthomonas pathogens with differing the control of the genomes of two Xanthomonas pathogens with differing the c
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Nature 417-459-463 (2002).

-!- FUNCTION: Catalyzes the ATP-dependent amination of UTP to example of nitrogen ()
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TIGKPAMs; TIGK00337; ByrG; 1.
PROSITE; PS00442; GATASE TYPE I;
Pyrimidine biosynthesis; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: Homotetramer (By similarity).
-!- SIMILARITY: Belongs to the CTP synthase family.
-!- SIMILARITY: Contains i type-1 glutamine amidotransferase
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MEDLINE=22022145; PubMed=10204217;

da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   either L-glutamine or ammonia as the source of nitrogen (similarity).

CATALYTIC ACTIVITY: ATP + UTP + NH(3) = ADP + phosphate + ENZYME REGULATION: Allosterically activated by GTP, when is the substrate. Inhibited by CTP (By similarity).

PATHWAY: Pyrimidine biosynthesis; conversion of UMP to CT
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                                                                                                                                                                                             MTKFIFITGGVVSSLGKGIAASSLAAILEDRGLKVTITKLDFYINVDFGTMSFFOHGEVF
                                                                                                                                                                       MTPLIFVTGGVVSSLGKGIAAASLASILEARGLKYTMMKLDPYINVDPGTMSPPQHGEVY
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                                                                                                                                                                                                                                                                  Score 1931; Di
Pred. No. 1.2e
79; Mismatches
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GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMINATOR DOMAIN
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    Glutamine amidotransferase;

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.2e-113;
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                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio vulnificus.
Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tyrg VIEVU STANDARD; PRT; 545 AA.

Q8DC63;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
CTP synthase (EC 6.3.4.2) (UTP--ammonia ligase)
PYRG OR VV11578.
                                                                                                                                                                                                                                                                                                                                                                             Rhee
Choy
    HAMAP;
                                                                                                                                                                                                                                                                                                              "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases:
-i-FUNCTION: Catalyzes the ATP-dagendent amination of UTP teither L-glutamine or ammonia as the source of nitrogen
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CMCP6;
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                               (last) step.
SUBUNIT: Homotetramer (By similarity).
SIMILARITY: Belongs to the CTP synthase family.
SIMILARITY: Contains i type-1 glutamine amidotransferase domain.
                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: ATP + UTP + NH(3) = ADP + phosphate + ENZYME REGULATION: Aliosterically activated by GTP, when g is the substrate. Inhibited by CTP (By similarity).

PATHWAY: Pyrimidine biosynthesis; conversion of UMP to CTP
                                                                                                                                                                                                                                                                                                 similarity.
                                                                                                                                                                                                                                                                                                                                                                             J.H., Kim S.Y.,
H.E.;
 AE016802; AA010002.1;
'; MF_01227; -; 1.
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PROSITE; PS00442; GATASE TYPE I; 1.
Pyrimidine biosynthesis; Ligase; Glutamine amidotransferase;
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InterPro; IPR004468; PyrG.
Pfam; PF00117; GATase; 1.
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KAGLKVSGLSADKKLVEMIENPNHPWFVAAQFHPBFTSTPRDGHPLFSGFIKAAGEN
             AAGMKFSGKSLDGRLVBIIELPEHPWFLACQPHPBFTSTPRWGHALFSGFVEAAAKH
                                             GENVRDESSDLGGTWRLGAQXCRLKADSLAPQLYQKDVITERHRHRVEFUNQYLKQLE

| GENVBERTESSNLGGTWRLGSQLCHLAKGTKARELYGSDTHERHRHRVEVNNNLRPQIB
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::|||||:|||||||:|
LAAKYARENKVPYLGICLGMQVALIEYARNVAGMEGAHSTEFNKDTKYPVVGLITEWVDS
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GUUTAMING AMIDOTRANSFERASE
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1925; DB 1;
Pred. No. 2.8e-113;
0; Mismatches 97;
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RESULT 8
PYRG VIBCH
ID PYRG V
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CTP synthase
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 SEQUENCE FROM N.A.
STRAIN=El Tor N16961 / Serotype O1;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson
                                                                                                                  Vibrio cholerae
                                                                                                                                                                                                                     PYRG_VIBCH
                                                                      NCBI_TaxID=666;
                                                                                     Vibrionaceae; Vibrio
                                                                                                    Bacteria; Proteobacteria;
                                                                                                                               OR VC2448
                                                                                                                                            (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
(Rel. 41, Last annotation ligase)
                                                                                                                                                                                                                     STANDARD;
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   w.c.,
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    R.A.,
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Gill S.
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InterPro; IPR000991; GATase_1
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-!- FUNCTION: Catalyzes the ATP-dependent either L-glutamine or ammonia as the s
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Fraser C.M.;
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Pyrimidine
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SIMILARITY: Belongs to the CTP synthase
SIMILARITY: Contains 1 type-1 glutamine
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CATALYTIC ACTIVITY: ATP + UTP + NH(3) = ADP + phosphate + CTP.

ENZYME REGULATION: Allosterically activated by GTP, when glutaming the substrate. Inhibited by CTP (By similarity).

PATHANY: Pyrimidine biosynthesis; conversion of UMP to CTP; third
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (last) step.
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ne biosynthesis; Ligase;
DAYKSVNEALKHAGLKNRLSVTIKYVDSQDVETKGTDVLNGLDAILVPGGFGDRGIEGKI
                                    DAYKSLNEALIHAGIHTRHKVQISYIDSETIEAEGTAKLKNVDAILVPGGFGERGVEGKI
                                                                                                                                 :||:|| |: | |||||| : :: | |||| ||:|: :|| |||:|: :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :
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AMINATOR DOMAIN.

GLUTAMINE AMIDOTRANSFERASE.

GATASE (BY SIMILARITY).

GATASE (BY SIMILARITY).

GATASE (BY SIMILARITY).
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    Glutamine amidotransferase;

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                                                                                                                                                                                                             EMBL; AB006225; AAK03956.1; --
HAMAP; MF 01227; -; 1
InterPro; IPR000991; GATase 1.
InterPro; IPR004468; PyrG.
Pfam; PF00117; GATase; 1.
                                                                                                                                                                 TIGRFAMS; TIGR00337; PyrG; 1.
PROSITE; PS00442; GATASE_TYPE_I;
Pyrimidine biosynthesis; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapu "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-!- FUNCTION: Catalyzes the ATP-dependent amination of UTP to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotation update)
28-FEB-2003 (Rel. 41, Last amotation update)
CTP synthase (EC 6.3.4.2) (UTP--ammonia ligase)
                                                                                                                                        DOMAIN
                                                                                                                                                       Complete

    -!- SIMILARITY: Belongs to the CTP synthase family.
    -!- SIMILARITY: Contains 1 type-1 glutamine amidotransferase

                                                                                                                                                                                                                                                                                                                                                                                                                                                                {last) step,
-!- SUBUNIT: Homotetramer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PASMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: ATP + UTP + NH(3) = ADP + phosphate + ENZYME REGULATION: Allosterically activated by GTP, when g is the substrate. Inhibited by CTP (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        either L-glutamine or ammonia
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                 Similarity
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                                                            301
379
515
517
542 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pyrimidine biosynthesis; conversion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pasteurella.
              68.8%;
                                                               3
                                                            AMINATOR DOMAIN.
GLUTAMINE AMIDOTRANSFERASE.
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
C2A72913A502F612 CRC64;
             Score 1918;
Pred. No. 7.
 Mismatches 101;
                                                                                                                                                                    1.
Glutamine
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                             Length 542;
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P08398;
01-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECOLI
    Science
[3]
                                                                  SPECIES=E.coli; STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattine=F.R., Delunkett G. III, Bloch C.A., Perna N.T., Burl
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYRG OR B2780 OR C3345 OR
Escherichia coli,
Escherichia coli 06,
Escherichia coli 0157:H7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1988 (Rel. 08, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
CTP synthase (RC 6.3.4.2) (UTP--ammonia ligase) (CTP synthese)
PYRG OR B780 OR C3345 OR Z4095 OR ECS3640 OR SF2795.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992, 83334, 623;
                                                                                                                                                                                                                                                                                  synthetase."
                                                                                                                                                                                                                                                                                                                              WEDLINE=86168304;
Weng M., Makaroff
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shigella flexneri.
                           The complete genome sequence of Science 277:1453-1474(1997).
                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        "Nucleotide sequence
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                                                                                                                                                                                                                                                                 Chem.
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C.A., Zalkin H.
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Escherichia
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                                                   Escherichia coli K-12.";
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SEQUENCE OF 1-12.

SEQUENCE OF 1-12.

SPECIES=S.coli; STRAIN=K12 / EMG2;

SPECIES=97443975; PubMed=9298646;

MEDLINE=97443975; PubMed=9298646;

Link A.U., Robisson K., Church G.M.;

"Comparing the predicted and observed properties in the genome of Escherichia coli K-12.";

Flectrophoresis 18:1259-1313(1997).
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Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=S.flexmeri; STRAIN=301 / Serotype 2a; MEDLINB=22772406; PubMed=12384590; Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang Yang J., Yang G., Wu H., Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wer Y., Zho B., He B., Chen R., Ma D., Qiang B., Wer Y., Zho B., He B., Chen R., Ma D., Qiang B., Wer Y., Zho B., He B., Chen R., Ma D., Qiang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Lang B., Wer Y., Zho B., Lang B., Lang B., Wer Y., Zho B., Lang B., Lang B., Wer Y., Zho B., Lang B., Lang B., Wer Y., Zho B., Lang B., Wer Y., Zho B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., Lang B., 
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SPECIES=E.coli; STRAIN=0157:H7 / RIMD 0509952;

SPECIES=E.coli; STRAIN=015796;

MEDLINE=21156231, PubMed=11258796;

MEDLINE=21156231, PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe 1 Ida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunat Ida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunat Kuhara S., Shiba T., Hattori M., Shinagawa H.;

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.", DNA Res. 8:11-22(2001).
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SPECIES-E.COLI; STRAIN=0157:H7 / EDL933 / ATCC 700927;
SPECIES-E.COLI; STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINB=21074935 PubMed=11206551;
MEDLINB=21074935 PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.,
Welch R.A., Blattner F.R.,
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
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SPECIES=B.coli, STRAIN=06:H1 / CPT073 / ATCC 700928;

SPECIES=B.coli, STRAIN=06:H1 / CPT073 / ATCC 700928;

MEDLINE=22388234, PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,

Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna M.T.,

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

Mobley H.L.T., Schwartchia coli.";

Mobley H.L.T., Stroud D.,

Mobley H.L.T., Stroud D.,

Mobley H.L.T., Schwartchia coli.";

Mobley H.L.T., Schwartchia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
                                                                                                                                                                                                                                                                                                                                           "Structural role for a conserved r glutamine amide transfer domain."; J. Bacteriol. 169:3023-3028(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=E.coli;
MEDLINE=87250264;
                     ROLE OF GTP,
SPECIES=E.col
                                                                                                          Biochemistry
                                                                                                                                      synthetase.".
                                                                                                                                                                                              MEDLINE=93222179; PubMed=8385490; Robertson J.G., Villafranca J.J.;
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MEDLINE=21234865;
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                                                  AND MUTAGENESIS OF CYS-378.
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PubMed=11336655
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and 0157.";
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Tobe T.,
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Matches 363; Conservative
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HAMAP; MF 01227;
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InterPro; IPR000991; GATase_1.
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Biochem. J. 356:223-232(2001)
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PROSITE; PS00442;
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PS00442; GATASE_TYPE_I;
e biosynthesis; Ligase;
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Z
                                                                                                                                                  ACTIVITIES.

G->P: LOSS OF GLUTAMINE-DEPENDENT
ACTIVITY, BUT NO CHANGE IN AMMONIA-
DEPENDENT ACTIVITY.

C->A,S: LOSS OF GLUTAMINE-DEPENDENT
ACTIVITY, BUT NO CHANGE IN AMMONIA-
DEPENDENT ACTIVITY.

V -> L (IN REF. 1).

M -> S (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                        AMINATOR DOMAIN.
GLUTAMINE AMIDOTRANSFERASE.
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
CATASE (BY SIMILARITY).
V-S: 30% INCREASE IN BOTH GLUTAM
DEPENDENT AND AMMONIA-DEPENDENT
                                         Score 1916; DB Pred. No. 1e-112
                                                                                                                             EA342793545355FC CRC64;
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                 Mismatches

    Glutamine amidotransferase;

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                            MEDIANE-2117863, PubMedi2142430;

Deng W., Burland V., Plunkett G. III, Boutin A., Merian N.T., Rose D.J., Mau B., Zhou S., Schwartz E. Fetherston J.D., Lindler T.E., Brubaket R.R., Plant Fetherston J.D., Lindler M.A., Nilles M.L., Matson
                                                                                                                                                                   STRAIN=CO-92 / Biovar Orientalis;

MEDLINE=21470413; PubMed=11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaibia M., James K.D., Churcher C., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Genome sequence of Yersinia pestis, the causative agent of plague
                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
CTP synthase (EC 5.3.4.2) (UTP--ammonia ligase)
PYRG OR YPO3377 OR Y0813.
               Straley S.C.,
Perry R.D.;
                                                                                                           SEQUENCE FROM N.A.
STRAIN=KIM5 / Biovar Mediaevalis;
                                                                                                                                                                                                                                                                                                                                                                                    Bactería; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Yersinia,
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                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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413:523-527(2001).
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-: FUNCTION: Catalyzes the ATP-dependent amination of UTP to either L-glutamine or ammonia as the source of nitrogen (E similarity).

-: CATALYTIC ACTIVITY: ATP + UTP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + UTP + ATP + UTP + CATALYTIC ACTIVITY: ATP + UTP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + UTP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + UTP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + UTP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + CATALYTIC ACTIVITY: ATP + NH(3) = ADP + phosphate + NH(3) + NH(4) + NH(4) + NH(4) + NH(4) + NH(4) + NH(4) + NH(4) + NH(4) + NH(4) + NH(4) + NH(4) + NH(4) + NH(4) + NH(4) + NH(4) + NH(4) +
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EMBL; AE013684; AAM84400.1; -.
PIR; AC0410; AC0410.
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SIMILARITY: Belongs to the CTP synthase family.
SIMILARITY: Contains 1 type-1 glutamine amidotransferase
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ine biosynthesis; Ligase; Glutamine amidotransferase;
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GAUTAMINE AMIDOTRANSPERASE
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CTP synthase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYRG HAEIN
DOMAIN
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PIR; F64181; P64181.
TIGR; HI1077; --
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                                                                                                                                                                                                                                                  HAMAP; MF 01227; -; 1.
InterPro; IPR000991; GATase_1.
InterPro; IPR004468; PyrG.
                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 269:496-512(1995).
-!- FUNCTION: Catalyzes the ATP-dependent amination of UTP to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC
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                                                                                                                                                            Pyrimidine biosynthesis; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Whole-genome random sequencing
                                                                                                                                         Complete
                                                                                                                                                                                                                                 fam; PF00117; GATase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (last) step.
SUBUNIT: Homotetramer (By similarity).
SIMILARITY: Belongs to the CTP synthase family.
SIMILARITY: Contains I type-1 glutamine amidotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: ATP + UTP + NH(3) = ADP + phosphate + ENZYMB REGULATION: Allosterically activated by GTP, when 9 is the substrate. Inhibited by GTP (By similarity).

PATHWAY: Pyrimidine biosynthesis; conversion of UMP to CTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity)
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t annotation update)
(UTP--ammonia ligase)
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                   AMINATOR DOMAIN.
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    Glutamine amidotransferase;

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                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce,
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Merrick J.M.,
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            MEDIINE-20365717; PubMed-10910347;

RX Simpson A.J.G., Reinach F.C., Arrida P., Abreu F.A., Acencio M.,

RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,

RA Alvarenga R., Alves L.M.C., Araya J.E., Bove J.M., Briones M.R.S.,

RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,

ROClauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,

RA Colauto N.B., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,

RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,

RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,

RA Fagia J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,

RA Faga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,

RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,

RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper B.L., Kitajina J.P.,

RA Krieger J.E., Kuranae E.E., Laigret F., Lambais M.R., Leite L.C.C.,

RA Macques M.V., Martins E.A.L., Martins S.M.F., Matsukuma A.Y.,

RA Marques M.V., Martins E.A.L., Martins S.M.F., Matsukuma A.Y.,

RA Marques M.V., Martins E.A.L., Martins S.M.F., Matsukuma A.Y.,

Marchado M.A., Madeira A.M.B.N., Matsukuma A.Y.,

Martins E.A.L., Martins S.M.F., Matsukuma A.Y.,

Martins C.Y., Monteiro-Vitorello C.B.,
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Best Local Simi
Matches 364;
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
CTP synthase (EC 6.3.4.2) (UTP--armonia ligase)
                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Xanthomonadaceae; Xylella
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InterPro; IPR000991; GATase_1.
InterPro; IPR004468; PyrG.
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Local tocal;
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                                                                                                                                                                      VTEDGAETDLDLGHYERFLKTTWTKKNNFTTGQVYEQVLKNERKGDYLGATVQVIPHITD 120
                                                                                                                SAGELKTKPTQHSVKELRTIGIQPDILICRSEQPIPASERRKIALFTNVÆEKAVISAIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteome.
                      DVLYGMPLELRRQGLDEIVIDQFKLSGTASLADLSEWEDVVDAIKHPLDEVTIAVVGKYV
                                                         DTIYRIPLLIREQGLDDLVVDQLRLDVPA--ADLSAWEKVVDGLTHPTDEVSIAIVGKYV 298
                                                                                                                                                                                                                                                VIDDGABTDLDLGHYERFVRTRLSRNNSVTTGRIYQNVICKERGDYLGATVQVIPHITD
                                                                                              AAGELKTKPTOHSVKELRSIGIOPDVLLCRSEQVIPDSERRKIALFTNVSERAVIGCPDI
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Pred. No. 5.1e-112;
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Length

4

240

120

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WA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
A Mhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
A Mhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
A de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
A Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
A Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
A da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
A da Silva A.C.R., da Silva M.M., Jr., Siqueira W.J., de Souza A.A.,
A da Silva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A da Silva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A da Silva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A Zago M.A., Zatz M., Meidanis J., Setubal J.C.,
The genome sequence of the plant pathogen Xylella fastidiosa.";
The genome sequence of the plant pathogen Xylella fastidiosa.";
The genome sequence of the plant pathogen Xylella fastidiosa.";
C either J-glutamine or ammonia as the source of nitrogen (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (last) step.
-!- SUBUNIT: Homotetramer (By similarity).
-!- SIMILARITY: Belongs to the CTP synthase family.
-!- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).

-:- CATALYTIC ACTIVITY: ATP + UTP + NH(3) = ADP + phosphate
-:- ENZYME REGULATION: Allosterically activated by GTP, wher
is the substrate. Inhibited by CTP (By similarity).
-:- PATHWAY: Pyrimidine biosynthesis; conversion of UMP to C
                                                                                                                                                                                                                                                                                                                             Pfam; PP00117; GATase; 1.
TICRFAMs; TICR00337; ByrG; 1.
PROSITE; PS00442; GATASE TYPE I; 1.
Pyrimidine biosynthesis; Ligase; Glutamine amidotransferase;
                                  AMINATOR DOMAIN.
GLUTAMINE AMIDOTEANSFERASE.
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
5EE8769917043811 CRC64;
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RESULT 14
PYRG_NEIMA
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MEDINE=2022556; PubMed=10761919;

Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd

Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

Whitehead S., Spratt B.G., Barrell B.G.;

"Complete DNA sequence of a serogroup A strain of Neisseria

meningitidis 22491.";

Nature 404:52-506(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
CTP synthase (EC 6.3.4.2) (UTP--ammonia ligase)
PYRG OR NMA1742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYRG NEIMA
Q9JTK1;
                            EMBL; AL162757; CAB84970.1;
PIR; F81798; F81798.
HAMAP; MF 01227; -; 1.
                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            similarity).

CAPALYTIC ACTIVITY: ATP + UTP + NH(3) = ADP + phosphate + CTP.

ENZYME REGULATION: Allosterically activated by GTP, when glutamine
is the substrate. Inhibited by CTP (3y similarity).

PATHWAY: Pyrimidine biosynthesis; conversion of UMP to CTP; third
                                                                                                                                                                                                                                           SUBUNIT: Homotetramer (By similarity).
SIMILARITY: Belongs to the CTP synthase family.
SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Catalyzes the ATP-dependent amination of UTP to either L-glutamine or ammonia as the source of nitrogen (
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                IPR000991;
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PYRG NEIMB
ID PYRG NE
AC Q9JYJB
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DT 28-FEB
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                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
CTP synthase (EC 6.3.4.2) (UTP--ammonia ligas
PYRG OR NMB1554.
                                                                                                                                              PYRG_NEIMB
Q9JYJ8;
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ACT SITE
 SEQUENCE FROM N.A. STRAIN=MC58 / Serc
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PROSITE; PS00442; GATASE TYPE I;
Pyrimidine biosynthesis; Ligase;
                                                  Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
                                                                        Neisseria meningitidis (serogroup B)
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GAUTAMINE AMIDOTRANSFERASE
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
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Glutamine
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TIGREAMs; TIGR00337; PYTG; 1.
PROSITE; PS00442; GATASE TYPE I; 1.
Pyrimidine biosynthesis; Ligase; Glutamine amidotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; NMB1554; --; 1.
HAMAP; MF_01227; --; 1.
InterPro; IPR000991; GATase 1.
InterPro; IPR004468; PyrG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (last) step.
-!- SUBUNIT: Homotetramer (By similarity).
-!- SIMILARITY: Belongs to the CTP synthase family.
-!- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete
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Science 287:1809-1815(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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CATALYTIC ACTIVITY: ATP + UTP + NH(3) = ADP + phosphate + CTP.

ENZYME REGULATION: Allosterically activated by GTP, when glutamine is the substrate. Inhibited by CTP (By similarity).

PATHWAY: Pyrimidine biosynthesis; conversion of UMP to CTP; third
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                     SAGELKTKPTQHSVKELRTIGIQPDILICRSEQPIPASERRKIALFTNVAEKAVISAIDA 240
                                                                                                                                                                                                                 EIKRRYYESAEGKDVALIEVGGTVGDIESLPFLETIROMGVELGRDRALFIHLTLYPYIK 180
                                                                                                                                                                                                                                                                                                                                                                              VTEDGAETDLDLGHYERFLKTTMTKKNNFTTGQVYEQVLRNERKGDYLGATVQVTEHITD 120
DSIYECPEMIHDQGIDNIITEQLQLAVQQADLTAWKKIVHAIQNPKHTVKIAMVGKYVDL
                                                    DTIYRIPLLIREQGLDDLVVDQLRLDVPAADLSAWEKVVDGLTHPTDEVSIAIVGKYVDH 300
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Pred. No. 5.46
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GLUTAMINE ANIDOTRANSFERASE.
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
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541 NK 542
                                                  481 TLEQAGLVIGGVSAGRERLVETIELPNHPWFFACQFHPEFTSNPRKGHPLFTAFVKAALN
                                                                                                                                                                                                   QLEAAGMKFSGKSLD-GRLVBIIELPEHPWFLACQFHPEPTSTPRNGHALFSGFVEAAAK 537
                                                                                                               MDEAGELVTRDEDSDLGGTWRLGAQKCRLKADSLAFQLYQKDVITERHRHRYEFNNQYLK 478
                       HX 539
                                                                                                   QTADGSVETRDESTDLGGTMRLGAQEVELKAGSLAAKIYGSGHIRERHRHRYEVNNNYVP
                                                                                                                                                    GKIAAVRYARENNVPYLGICLGMQIALIEYARDVAGLKGANSTEFDLKCAAPVVALIDEW
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Search completed: January 29, 2004, 15:50:42 Job time: 11.244 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                   SPTREMBL 23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
4: sp_human:*
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Gapop 10.0 , Gapext 0.5
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2788
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Copyright (c) 1993 - 2004 Compugen Ltd.
SUMMARIES
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Q8ftl2 corynebacte	Q8FTL2	16	559	49.4	1377	16
Q8gdz6 heliobacill	Q8GDZ6	N	468	50.8	1416.5	15
Q8g5x7 bifidobacte	Q8G5X7	16	553	51.4	1432.5	14
Q8dwg1 streptococc	Q8DWG1	16	536	54.3	1514	13
Q8f3j3 leptospira	Q8F3J3	16	542	54.9	1532	12
Q8e290 streptococc	Q8E290	16	534	54.9	1532	11
Q8e7p8 streptococc	Q8 E7 P8	16	534	55.0	1533	10
Q8dkt7 synechococc	Q8DKT7	16	543	55.8	1555.5	φ
_	OXDQYO	16	535	56.0	1561	80
QBcni2 staphylococ	QBCN12	16	535	56.5	1575	7
Q8g0g1 brucella su	19098 0	16	542	56.9	1585	0,
Q8em53 oceanobacil	Q8EM53	16	535	57.9	1614	U
Q8d2k0 wiggleswort	Q8D2K0	16	552	59.6	1662	4.
Q8ge64 aeromonas h	QBGE64	Ŋ	498	62.3	1738	ω
Q8ebq9 shewanella	6 Č BZ8 Č	16	546	69.0	1925	Ŋ
Q8dc63 vibrio vuln	Q8DC63	16	545	69.0	1925	فيو
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ტ. ნ	7.9	7.9	11.0	33.0	33.4	36.1	36.3	37.6	39.2	40.0	41.2	41.8	41.9	42.6	43.3	43.5	43.9	43.9	43.9	44.0	44.0	44.4	44.8	44.9	45.6	46.2	46.5	47.8
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Q9L211	Q911K5	Q9H6Q0	QBUJKI	Q8SQI7	Q9BRI0	Q9VUL1	Q27725	Q8ILZ3	Q9NBX8	Q9XXXII	074638	042644	Q8EWZ8	OTOA60	Q27660	Q9H8K9	Q9NRF8	P70303	Q9H8O9	Q9ASG9	Q8RZH3	065445	064753	Q9SY26	Q922Y4	004252	SMLT6D	Q8L6Z9
Q91211 streptomyce	Q9ilk5 pseudomonas		1	Q8sqi7 encephalito	Q9bri0 homo sapien			Q8ilz3 plasmodium		Q9xxml caenorhabdi	074638 gibberella	ຜ	Q8ewz8 mycoplasma	Q9vul0 drosophila	Q27660 giardia lam	Q9h8k9 homo sapien	Q9nrf8 homo sapien	P70303 mus musculu	2	_	Q8rzh3 oryza sativ				Q922y4 mus musculu	Ωı		Q816z9 arabidopsis

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	RALFIHLTLVP	63 TEDGAETOLDLGHYERFIRTKWITKRNNFTAGRVYSDVLAKERRGDYLGATIQVIPHITND 122	62 TEDGAETDIDIGHYERFIKTTMTKKNNFTTGQVYBQVIRNERKGDYLGATVQVIPHITDE 121	3 TNYIFVTGGVVSSLGKGIAAASLAAILEARGLKVTMMKLDEVINVDEGTMSPTQHGEVFV 62	SLAAILEDRGLKVI	Query Match 69.0%; Score 1925; DB 16; Length 545; Best Local Similarity 67.0%; Pred. No. 2e-125; Matches 360; Conservative 80; Mismatches 97; Indels 0; Gaps 0;		Complete proteome.	ted (DEC-2002) to the	genome sequence of Vibrio vulnificus		Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,	MC PC	SEQUENCE FROM N.A.	[1]	NCBI TaxID=672;	eae; Vibrio.	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;	Vibrio vulnificus,	VV11576.		(TrEMBLrel. 23, Last annotation	(TrEMBLrel. 23,	-2003 (TrEMBLrel.		Q8DC63 PRELIMINARY; PRT; 545 AA.	53 1 · · · · · · · · · · · · · · · · · ·

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Q8EBQ9;
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Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C. Read T.D., Eisen J.A., Seshadri R., Ward, M., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanam, W. Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., DeBoy R.T., Deterson J.D., Umayam L.A., White O., Wolf A.M., Wandthevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Peldblyum T.V., Smith H.C., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium
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CTP synthase.
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Q8GE64;
01-MAR-2003
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Sha J., Galindo C.L., Pancholi V., Popov V.L., Chopra A.K.;
Sha J., Galindo C.L., Pancholi V., Popov V.L., Chopra A.K.;
"Identification of a Potentially New Virulence Gene Enolase the Differentially Expressed under in vitro versus in vivo Growth Conditions in Aeromonas hydrophila.";
Conditions in Aeromonas hydrophila.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AV141757; AAN28925.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aeromonas hydrophila.
Bacteria; Proteobacteria;
Aeromonadaceae; Aeromonas.
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70; Mismatches 97;
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Q8D2K0;
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01-MAR-2003 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wigglesworthia brevipalpis.
Bacteria, Proteobacteria, Gammaproteobacteria,
Enternbacteriaceae, Wigglesworthia.
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552 AA;
VRFARENKIPYLGICLGMOSAVIEFARNVVGLEGAHSTEFLPKSPHPVIGLITEMMDEAG
                                                                                 YKSLNEALIHAGIHTRHKVQISYIDSETIEAEGTAKLKNVDAILVPGGFGERGVEGKIST
                                                                                                                                                                                                                                               ELKTKPTQHSVKELRTIGIQPDILICRSEQPIPASERRKIALFTNVAEKAVISAIDADTI 243
                                                                                                                                                                                                                                                                                                   KCIINAGKGFDILLVEIGGTVGDIESLPFLESIROMSIEIGKNKILYIHLTLVPYLKISK 190
                                                                                                                                                                                                                                                                                                                            RRVYESAEGKDVALIEVGGTVGDIESLPFLETIRQMGVELGRDRALFIHLTLVPYIKSAG 183
                                                                                                                                                                                                                                                                                                                                                                                                                        DGAETDLDLGHYERFLKTTWIKKNNFTTGQVYEQVLRNERKGDYLGATVQVIPHITDBIK 123
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                                                           YRSLISALEHAGLKNRLMINIQLINSKKIBSLGISCLKNLHAILIPGGFGYRGVEGKIIA
                                                                                                                                           YKIPILIKKQGLDSYVCDRFCIKRPEADLSKWKEVIYKQKNPLGNVNIGIIGKYTELPDS
                                                                                                                                                                                 YRIPLLIREQGLDDLVVDQLRLDVPAADLSAWEKVVDGLTHPTDEVSIAIVGKYVDHTDA 303
                                                                                                                                                                                                                          EVKTKPTQHSVKELLSIGIQPDILICRSEKNVSKYEKSKIALFCNVPKQAVFSLKNTNSI
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Last annotation update)
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Pred. No. 4.1e-107;
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Best Local S
Matches 310
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STRALN=HTB831 / DSM 14371 / JCM 11309;

MEDLINE=22220767; PubMed=12235376;

Takani H., Takaki Y., Uchiyama I.;

"Genome sequence of Oceanobacillus iheyensis isolated from "Genome sequence of Oceanobacilus iheyensis isolated from Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP004603; BAC14963.1; -.
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01.MAR-2003 (TrEMBLrel. 23, Last sequence update)
01.MAR-2003 (TrEMBLrel. 23, Last sequence update)
01.MAR-2003 (TrEMBLrel. 23, Last sequence update)
CTP synthase (UTP-ammonia ligase) (EC 6.3.4.2).
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  WMDBAGBIVTRDEDSDLGGTWRLGAQKCRLKADSLAFQLYQ-KDVITERHRHRYEFNNQY
                                          DGKIEAIRYARENNI PFFGICLGMQLASVEFARNVVGLSQAHSAEINPHTPHPVIDLLPE
                                                                  EGKISTVRFARENKIPYLGICLGMQSAVIEFARNVVGLEGAHSTEFLPKSPHPVIGLITE
                                                                                                                       ELPDAYLSVVESLKHAGYDYDTDVKIHWINSELLSEEQIKEELSKVDGVLVPGGFGDRGI
                                                                                                                                             DHTDAYKSLNEALIHAGIHTRHKVQISYIDSETI-EAEGTAKLKNVDAILVPGGFGERGV
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Q8G0G1;
01-MAR-2003
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STRAIN=1330 / Biovar 1;

STRAIN=1330 / Biovar 1;

MEDLINES=2247741; PubMed=12271122;

Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,

Read T.D., Dodson R.J., Umayam L., Brinkec L.M., Beanan M.J.,

Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,

Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,

Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,

Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,

Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;

"The Brucella suis genome reveals fundamental similarities between

animal and plant pathogens and symbionts.";

Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
SEQUENCE 542 AA; 60058 MW;
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Brucella suis.
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GKISTVRFARENKIPYLGICLGMQSAVIBFARNVVGLEGAHSTEFLPKSPHPVIGLITEW
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                                                                          LKDAYKSLIEALHIGGLANKVKVNLDWIEAQVFESEDPAPYLEKVHGILVPGGFGERGAE
                                                                                                               HTDAYKSLNEALIHAGIHTRHKVQISYIDSETIEAEGTAK-LKNVDAILVPGGFGERGVE
                                                                                                                                                                   ATIYDVPIAYHKEGLDSEVLSAFGIDPAPKPRMDRWEEVSHRLHNPEGEVTIAVVGKYTG
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                                                                                                                                                                                                                                                            AAGELKTKPTQHSVKELRSIGIAPDILLVRADREIPESERRKLSLFCNVRESAVIQALDV
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Pred. No. 8.9e-102;
8; Mismatches 143;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
CTP synthase.
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Chen Z., Wen Y.;
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Bacteria; Firmicutes; Bacillales;
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                           REQLESNGMVFSGTSPDGRLVEITEIPKNDFFTACQFHPEFLSRPNRPQPTFKSFVEAAL
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Pred. No. 4.3e-101;
5; Mismatches 132;
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MEDLINE=21429245; FUDMed=11544234;

Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett !

Hoskins J., Alborn W.E. Jr., Fritz L., Fu D.-J., Fuller W., Geringe:

DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringe:

Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,

LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,

McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,

Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,

Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,

Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome of the bacterium Streptococcus J. Bacteriol. 183:5709-5717(2001).
MBL; AE008423; AAK99242.1; -.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
CTP synthetase (EC 6.3.4.2).
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Makamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto Makamura Y., Kaneko T., Sato S., Kimura T., Kishida Y., Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
DNA Res. 9:123-130(2002)
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Bacteria; Cyanobacteria;
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Hypothetical protein; Complete
SEQUENCE 534 AA; 59294 MW;
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Bacteria; Firmicutes; Lactobacillales;
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Mol. Microbiol. 45:1499-1513(2002)
EMBL; AL766843; CAD45751.1; -.
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CTP synthase.
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Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S. Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinket L.M., Daugherty S.C., Madoff L.C., Wolf A.M., Beanan M.J., Brinket L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonsy J.F., Madupu R., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora Jacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G., Fraser C.M.;
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Proc. Natl. Acad. Sci. U.S.A.
EMBL; AE014196; AAM99015.1; -.
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Hacteria: Firmicutes; Lactobaciliales; Streptococcaceae;
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Ligase; Complete proteome.
SEQUENCE 542 AA; 61024 MW; 80BF9D8BF864AF8A CRC64;
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MEDILIME=22295063; PubMed=12397186;
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S.,
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti
"Genome sequence of Streptococcus mutans UA159, a cariogenic c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl Acad Sci. U.S.A. 99:14434-14439(2002)
EMBL; AE01466; AAN57880.1; -.
Ligase; Lyase; Complete proceome.
SEQUENCE 536 AA; 59491 MW; 1512BADCEDBF8448 CR
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01-MAR-2003 (TrEMBLrel. 23,
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               ROOFEEAGFVESGVSPDNRLVEVVELSDKKFFVAAQYHPELQSRPNRPEELYTAFITAAV
                                   LKQLEAAGMKFSGKSLDGRLVEIIELPEHPWFLACQFHPEFTSTPRNGHALFSGFVEAAA
                                                                                       WMDEAGELVTRDEDSDLGGTMRLGAQKCRLKADSLAFQLY-QKDVITERHRHRYEFNNQY 476
                                                                                                                                               EGKISTVRFARENKIPYLGICLGMQSAVIEFARNVVGLEGAHSTEFLPKSPHPVIGLITE
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                                                                    QID-----IEDMGGTLRLGLYPCKLKSGSKTASAYSNQEVVQRRHRHRYEFNNAF
                                                                                                                                                                                                                DHTDAYKSLNEALIHAGIHTRHKVQISYIDSETIEAEG-TAKLKNVDAILVPGGFGERGV 357
                                                                                                                                                                                                                                              DVDHLYQIPLNLQAQNMDQIVCDHLKLDVPVADMTEWSAMVDKVMNLKKKTKIALVGKYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactobacillales;
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Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
EMBL; AE014709; AAN24687.1; -.
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Bacteria; Actinobacteria;
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Pessi G., Zwahlen M.-C., D
Pridmore R.D., Arigoni F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTEDGAETDLDLGHYERFLKTTMIKKNNFTTGQVYEQVLKNEKKGDYLGATVQVIPHITD 120
                                                                                                                                    WMD-EAGELVTRDEDSDLGGTMRLGAQKCRLKADSLAFQLYQKDVITERHRHRYEFNNQY
                                                                                                                                                                                                         CKIGALKFARETKLPALGLCLGLQSMVIEYSRHVLGIEDANSSEFEPDCANPVIATMEE
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADTIYRIPLLLREQGLDDLVVDQLRLDVPAADLSAWEKVVDGLTHPTDEVSIAIVGKYVD
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                                                 LKQLEAAGMKFSGKSLDGRLVEIIELPE--HPWFLACQFHPEFTSTPRNGHALFSGFVEA 534
                                                                                                        QKDIVAGK-
                                                                                                                                                                                                                                                           EGKISTVRFARENKIPYLGICLGMQSAVIEFARNVVGLEGAHSTEFLPKSPHPVIGLITE
                                                                                                                                                                                                                                                                                                            LPDAYLSVTEAIKAGGFANWAKVNVKWVAADRCETTEGAAAALDNVDGIVIPGGFGIRGI
                                                                                                                                                                                                                                                                                                                                                           HTDAYKSLNEALIHAGIHTRHKVQISYIDSETIB-AEG-TAKLKNVDAILVPGGFGERGV 357
                                                                                                                                                                                                                                                                                                                                                                                                                     APSIYDVPKILFEEGLDAYVVRELGLPFHDVDWDEWADLLERVHHPKHEVNIAIVGKYID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSAGELKTKPTOHSVKELRTIGIOPDILICRSEOPIPASERRKIALFTNVAEKAVISAID
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  KDRLREGGLR I SGQSPDGELTEFVELPQDVHPFYVATQAHPEFKSRPTKPHPLFAGLVKA
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                                                                                                      -GOMGHTMRIGSYPAELEEGSLVAELYGTTHVTERHRHRYEVNVAY
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Desiere F., Bork P.,
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Last annotation updat
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ork P., Delley
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Matches 276
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
CTP synthase (EC 6.3.4.2) (Fragment)
Heliobaciilus mobilis.
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Q8GDZ6;
01-MAR-2003
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NON_TER
SEQUENCE
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EMBL; AY142825; AAN87429.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Raymond J., Zhaxybayeva O., Blankenship R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blankenship R.E.; "Whole-genome analysis of photosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINB=22337798; PubMed=12446909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=28064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Clostridia; Clostridiales; Heliobacteriaceae;
Heliobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 298:1616-1620(2002).
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                                                                                                                                                                                                                                                                                                                                                                                    LEDRGLKYTITKLDPYINVDPGTMSPFQHGEVFYTEDGAETDLDLGHYERFLKTTMTKKN
                CRLKADSLAFQLYQKDVITERHRHRYEFNNQYLKQLEAAGMKFSGKSLDGRLVEIIEL
                                                     VVEYGRNVLGWEDANSSEFSETTTHPVIDLLPEQKDV
                                                                        VIEFARNVVGLEGAHSTEFLEKSPHPVIGLITEMMDEAGELVTRDEDSDLGGTMRLGAQK 444
                                                                                                      HIYSADLEGAPPEDFLSDVDGILVPGGFGDRGIEGKISALRYARENKIPLIGICLGMQLA
                                                                                                                           YIDSETIE-AEGTAKLKNVDAILVPGGFGERGVEGKISTVRFARENKIPYLGICLGMQSA
                                                                                                                                                                                                                           ILICRSEQPIPASERRKIALFYNVAEKAVISAIDADTIYRIPLLLREQGLDDLVVDQLRL
                                                                                                                                                                                                                                                              DIESLPFLETIRQMGVELGRDRALFIHLTLVPYIKSAGELKTKPTQHSVKELRTIGIQPD
                                                                                                                                                                                                                                                                                                                  NVTTGKIYWSVISKERKGEYLGGTVQVIPHITNEIKERVLRVARESSPDVVITEIGGTVG
                                                                                                                                                                                                                                                                                                                                   NFTTGQVYEQVLRNERKGDYLGATVQVIPHITDEIKRRVYESA--EGKDVALIEVGGTVG
                                                                                                                                                        TCGEPDLKDWEALVHKIKNPKQQVTIGLVGXYVALPDAYMSVAESLRHAGIHHNASVKIK
                                                                                                                                                                                   DVPAADLSAWEKVVDGLTHPTDEVSIAIVGKYVDHTDAYKSLNEALIHAGIHTRHKVQIS
                                                                                                                                                                                                            IIVCRTEXAPPOELESKIALFCDIDPAAVIOMVDAETIYEVPLLLKKEELDDIVIBKLKL
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CRVNKGTKTWDAYQDEVIYERHRHRYEFNNNYREAIBKAGMIISGTSPDGRLVEVVEL
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Pred. No. 3.7e-90;
'3; Mismatches 116;
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                                                     BEKGGTMRLGIWA 410
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Search completed: January 29, 2004, 15:54:12 Job time : 42.5492 secs

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Database
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
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24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
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1623
1 MQIVLANPRGFCAGVDRAIE......GIEEKVVFSIPKELKKHMQA 318
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Result No.	Score	Query Match Length DB ID	ength	BB	ID	Description
,	1623	100.0	318	23	AAE22307	Methylomonas 16a s
N	1623	100.0	318	23	AAU80334	Methylomonas 16a O
ω	996	61.4	316	24	ABP60423	Escherichia coli L
4.	975	60.1	322	24	ABP77632	N. gonorrhoeae ami
ហ	969.5	59.7	349	20	AAY29260	Amino acid sequenc
σ	777	47.9	350	22	AAU58857	Propionibacterium
7	755	46.5	325	22	AAG90889	C glutamicum prote
œ	755	46.5	325	22	AAB78920	C. glutamicum SRT
ę	743.5	45.8	329	22	AAG81220	Mycobacterium tube

WPI; 2002-351711/38. N-PSDB; AAD35505.

Brzostowicz PC, Cheng Q, Odom JM, Picataggio SK,

Dicosimo DJ, Rouviere PE;

Koffas M,

Miller ES

01-SEP-2000; 2000US-229858P. 01-SEP-2000; 2000US-229907P.

(DUPO) DU PONT DE NEMOURS & CO E I.

04-SEP-2001; 2001WO-US27420.

4.	44	43	2	41	40	39	38	7	36	5	34	υ U	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	5	14	13	12	11	10	
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AAU61465	AAW73895	AAW26665	ABP73501	AAU35014	AAY23930	ABP40179	AAG82607	AAG81848	AAR13337	AAG81233	ABB48818	ABP66122	ABG24622	ABG18175	AAW20153	AAW20838	ABP99369	ABU51526	ABG13839	AAG37999	AAG26261	AAG38000	AAG26262	AAG38001	AAG26263	AAY15159	ABB47969	AAM51849	AAU67955	AAY37259	ABP66088	AAU09434	ABP62010	AAY35672	AAG81137	
Propionibacterium	east MEC3 protei	checkpoint	Candida albicans e		Consensus mino aci	Staphylococcus epi	S. epidermidis ope	S. epidermidis ope	HypB protein. Chl	Mycobacterium tube	Listeria monocytog	O		E.	H. pylori inner me	H. pylori inner me	Arabidopsis thalia	Helicobacter pylor							Arabidopsis thalia	A. palaestina LYTB	Listeria monocytog	P falciparum isopr	Propionibacterium	Amino acid sequenc	Bifidobacterium lo	lamydophila	C. pneumoniae BVH-	Chlamydia pneumoni	Mycobacterium tube	

ALIGNMENTS

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RESULT 1
AAE22307
                                                                                                                                                                           Carotenoid; isopentenyl pyrophosphate; antheraxanthin; astaxanthin; diet; anti-oxidant; steroid; flavour; fragrance; electro-optic application; aquaculture; enzyme; dimethylallyl diphosphate; lytB.
                                                                                                                                                          Methylomonas 16a sp.
                                                                                                                                                                                                                                                                         AAE22307 standard; Protein; 318 AA.
                                                                                                                      07-MAR-2002.
                                                                                                                                        WO200218617-A2.
                                                                                                                                                                                                                 Methylomonas 16a sp. dimethylallyl diphosphate (lytB) enzyme
                                                                                                                                                                                                                                    25-JUL-2002 (first entry)
                                                                                                                                                                                                                                                        AAE22307;
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RESULT 2
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ID AAUB
XX AAUB
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                                                                                            Methylomonas sp
                                                                                                                                                          Isoprenoid biosynthetic enzyme; isoprenoid compound; feed additive; keratenoid; pigment; flavour; fragrance; open reading frame 10; ORF10; lytB; IPP; isopentenyl diphosphate; dimethylallyl diphosphate.
                                                                                                                                                                                                                                                                                             Methylomonas 16a ORF10 lytB protein sequence.
                                                                                                                                                                                                                                                                                                                                                              15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU80334 standard; Protein; 318
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Pred. No. 2.3e-141;
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RESULT 3
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AC ABP6
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standard;

Protein;

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ABP60423;

31-MAR-2003

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                      encoding an isopremoid compound biosynthetic enzyme, and for the microbial production of isopremoid compounds. The molecules of the invention are also useful for regulating isopremoid biosynthesis in an organism and for producing recombinant organisms for producing various isopremoid compounds. The nucleic acid is also useful for feed additive, for the production of keratenoids and their derivatives, isopremoid intermediates, and as pure products useful as pigments, flavours and fragrances. The present amino acid sequence represents the Methylomonas 16a open reading frame 10 (ORF10) lyts protein of the invention, as described above. This sequence functions in the formation of IPP (isopentenyl diphosphate) and dimethylallyl diphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a new nucleic acid molecule an isoprenoid biosynthetic enzyme isolated from Methylomonas. The invention is useful for obtaining a nucleic acid molecule.
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Movel nucleic acid molecule encoding a isoprenoid biosynthetic enzyme, isolated from Methylomonas 16a, useful for the production of isoprenoid
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Pred. No. 2.3e-141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to enriching intermediates (A) in the mevalonate-independent isopremoid synthesis pathway (MEP-way) comprising deleting, inactivating or otherwise altering a gene (I) in the pathway, in a cell or organism, so that the enzymatic activity of the product of (I) is reduced or made non-natural. The method is used for production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (iii) as pharmaceuticals. Dead or live cells or organisms enriched in (A can be used similarly for treatment, in humans or animals, of asthma, Crohn's diseases, ulcerative colitis, multiple sclerosis, chronic bronchitis, (auto)immune diseases, allergies; bone diseases and osteoporosis, also a wide variety of other diseases and for improving the immune response against tumours. The present sequence is that of the Escherichia coli LytB protein, inactivated in examples of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (A), especially substrates of the GcpE and LytB enzymes that activate gamma/delta T cells. (A) and their derivatives are useful for:
(1) determining activity of GcpE and LytB, e.g. to identify their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 6-8; 10pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli; mevalonate-independent isoprenoid synthesis pathway; MEP-way; GcpE; LytB; T cell; asthma; Crohn's disease; multiple sclerosis; autoimmune disease; osteoporosis; tumour; antiasthmatic; antiulcer; antiinflammatory; neuroprotective; immunosuppressive; antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enriching intermediates in the mevalonate-independent pathway of isoprenoid synthesis, useful for therapeutic activation of T cells, comprises altering enzymatic activity in the pathway
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-0CT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteopathic; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli LytB protein SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (JOMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibitors;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to activate gamma/delta T cells; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2003-113392/11.
                                                                          181
                                                                                                              121
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                                                                                                                                                                                                                                                                                                                                          192;
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                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABZ59204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOMAA PHARMAKA GMBH
                                                                                                                                                                                    SEVPDGAILIPSAHGVSQAVRNEAKSRDITVFDATCPLVTKVHMEVARASRRGEESILIG
                                                                                                                                                                                                                                                                                    MQIVLANPRGFCAGVDRAIEIVDQAIEAFGAPIYVRHEVVHNRTVVDGLKQKGAVFIEBL 60
GKPAYLIDTYQDLKQDWLEGIEVVGVTAGASAPEVLVQEVIDQLKAWGGETTSVRENSGI
                                                                        DALREQFPSIKEQKKODICYATQNRQDAVHDLAKISDLILVVGSPNSSNSNRLREIAVQL
                                                                                                            HAGHPEVEGIMGQYS--NPEGGMYLVESPDDVWKLIVKNEEKLSFMTQTTLSVDDTSDVI 178
                                                                                                                                                HAGHPEVEGIMGOYEKCIEGGGIYLVEIPEDVRNLKVNNPNDLAYVIQITLSMIDIKVMV 180
                                                                                                                                                                                                                          SDVPVGSYLIFSAHGVSKEVQQEABERQLTVFDATCPLVTKVHMQVAKHAKQGREVILIG 120
                                                                                                                                                                                                                                                              MQILLANPRGFCAGVDRAISIVENALAIYGAPIYVRHEVVHNRYVVDSLRERGAIFIEQI
                                    DALRKREPKI VGPRKDDI CYATTNRQBAVRALABQABVVL VVGSKNSSNSNRLABLAQRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eberl M.
                                                                                                                                                                                                                                                                                                                                                                                                                    316 AA;
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                          61.4%;
61.3%;
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                                                                                                                                                                                                                                                                                                                                        Score 996; DB 24;
Pred. No. 1.8e-83;
9; Mismatches 58;
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RESULT 4
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                                                                                                                                                                                              Matches
                                                                                                                                                                                                         Query Match
Best Local &
                                                                                                                                                                                                                                                                  The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins a antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy sequences given in records ABP/6736-ABP81046 represent nucleic acid molecules of the invention.
                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                      New protein from Neisseria gonorrheae, useful for the manufacture medicament for treating or preventing N. gonorrheae infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N. gonorrhoeae amino acid
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                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-FEB-2001; 2001GB-0003424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200279243-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibacterial; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP77632;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fontana MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-FEB-2002; 2002WO-IB02069
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2003-058415/05
                       183
                                                126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239
                                                                                                                                                                                              192;
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                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             ABZ38602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHIRON SPA.
LNARFPNIRNPHKEDICYATTNROTAVKELAEQCDIVIVVGSPNSSNSNRLREVAASRGI
                      LREQFESIKEQKKODICYATQNRQDAVHDLAKISDLILVVGSENSSNSNRLREIAVQLGK
                                                           GHPEVEGTMGQYEKCTEGGGIYLVETPEDVRALKVANDADLAYVTQTTLSATDTKVMVDA
                                                                                              VPPGATEVYSAHGVSKAVQQEAAERGFRVFDATCPLVTKVHKEVARLDAQDCBIIMIGHK
                                                                                                                  VPVGSYLIFSAHGVSKEVQQEABBRQLTVFDATCPLVTKVHMQVAKHAKQGREVILIGHA 122
                                                                                                                                              IVLANPRGFCAGVDRAIEIVDQAIEAFGAPIYVRHEVVHNRTVVDGLKQKGAVFIEELSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EENIVFEVPKELR 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHAEVEGTMGQLAP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BEKVVFSIPKELK 313
                                                                                                                                                                                                                                              322 AA;
                                                                                                                                                                                                                                                                                                                                                                                Page 317; 815pp; English.
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein; 322
                                                                                                                                                                                                         60.1%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Masignani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence SEQ ID 1794.
                                                                                                                                                                                              48;
                                                -GXMLLVBTVGDVAKLEVRNPDKLAYVSQTTLSVDETKDIIAA
                                                                                                                                                                                                          Score 975;
Pred. No. 1.
                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy
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                                                                                                                                                                                                                    DB 24;
                                                                                                                                                                                                          6e-81;
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                                                                                                                                                      Best Local
Matches 1
                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                            sequence. P. aeruginosa is an opportunistic human pathogen present in soil water and plants. The specification describes virulence polypeptides and mucleic acid sequence encoding such polypeptides. These sequences can be used to identify a compound which is capable of decreasing the expression of a pathogenic virulence factor. Compounds that inhibit the expression or activity of virulence factor polypeptides can be used to treat pathogenic infections, especially where the infection is a P. aeruginosa infection.

note: the sequences given in the specification were poorly legible, and in some instances assumptions were made as to the identity of the residue; it is therefore possible that the sequence given below is
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 4; 228pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virulence factors useful in developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ausubel F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human pathogen; virulence polypeptide; virulence factor, pathogenic infection; Pseudomonas aeruginosa infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY29260 standard;
                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a Pseudomonas aeruginosa polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9927129-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                      entirely correct.
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                                                                                                                                                   191;
                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 દુ
                                            96
                                                                                                  36
                                                                                                                                                                   Similarity
HAGHPEVEGIMGQYEKCTEGGGIYLVETPEDVRNLKVNNPNDLAYVTQTTLSMTDIKVMV 180
                                                            SDVPVGSYLIFSAHGVSKEVQQEAEERQLTVFDATCPLVTKVHMQVAKHAKQGREVILIG 120
                                            DQVPDNVIVIFSAHGVSQAVRKSAEGRGLKVFDATCPLVTKVHMEVVRYSRDGHECVLIG 155
                                                                                               MQIKLAMPRGFCAGVDRAIBIVHRALDVFGPPIYVRHEVVHMKFVVDNLRQRGAIFVEBL
                                                                                                                           MOIVLANDRGECAGVDRAIBIVDQAIBAFGAPIYVRHEVVHNRTVVDGLKQKGAVFIBEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIVEVLPKELRR 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVVFSIPKELKK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAYMVDNASYLQRTWFEGKSKVGVTAGASAPEVLVREVLATIRGWGHET--VREGGGAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAYLIDTYQDLKQDWLEGIEVVGVTAGASAPEVLVQEVIDQLKAWGGETTSVRENSGIEB
                                                                                                                                                                                                            349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence
                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drenkard
Tsongalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of a virulence factor encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                  59.7%;
                                                                                                                                                     47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349
                                                                                                                                                     Score 969.5;
Pred. No. 5.9e
17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease treatments
                                                                                                                                                                   .9e-81;
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                                                                                                                                                                               DB 20;
                                                                                                                                                      72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mahajan-Miklos S;
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                                                                                                                                                                               Length 349;
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic CC polypeptides. The proteins and their associated DNA sequences are used in CC the treatment, prevention and diagnosis of medical conditions caused by CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne, CC pusculosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. CC P. acnes is also involved in infections of bone, joints and the central CC nervous system, however it is particularly involved in the inflammatory CC lesions associated with acne vulgaris. A method for detecting the CC presence or absence of P. acnes in a patient comprises contacting a CC sample with a binding agent that binds to the proteins of the invention CC and determining the amount of bound protein in the sample. The CC polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to CC downregulate expression and activity of P. acnes polypeptides and CC therefore treat P. acnes infections. The antibodies may also be used as CC diagnostic agents for determining P. acnes presence, for example, by CC enzyme linked immunosorbent assay (ELISA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgatis; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID No 20052; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                         treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L'maisonneuve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-APR-2000; 2000US-199047P
02-JUN-2000; 2000US-208841P
07-JUL-2000; 2000US-216747P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU58857 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-2001; 2001WO-US12865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes immunogenic protein #19753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-616774/71.
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                                                                                                                                                                                                                                                                                                                                                                                                                                AAS59596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORIXA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEMITFSMPKELR 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKPAYLIDTYQDLKQDWLEGIEVVGVTAGASAPEVLVQEVIDQLKAWGGETTSVRENSGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEKVVFSIPKELK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTPAYLIDGAEDMORGNFCGVRRIGITAGASAPEVLVRGVIAQLRENG--ASEEQELEGR
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO

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Matches 152
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Tateishi
                                    Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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                                                                                                                                                                carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; evolutionary study; environmental hazard; fermentation.
                                                                                                                                 Corynebacterium
                                                                                                                                                                                                                                                 Corynebacterium glutamicum; stress; resistance; tolerance;
                                                                                                                                                                                                                                                                                C. glutamicum SRT protein sequence SEQ ID NO:100.
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Note: The sequence data for this patent did not form specification, but was obtained in electronic format
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                                                                                                                                                                                                                                                                                                                                                                                     standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDALREQEPSIKEQKKDDICYATQNRQDAVHDLAKISDLILVVGSPNSSNSNRLREIAVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVPVGSYLIFSAHGVSKEVQQEAEERQLTVFDATCPLVTKVHMQVAKHAKQGREVILIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGADNAYLVDYARBIDPAWFEGVETIGISSGASVPEILVQGVIBRLAEFGYD--DVEEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGKP-AYLIDTYQDLKQDWLEGIEVVGVTAGASAPEVLVQEVIDQLKAWGGETTSVRENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRELKVKFPQLQDPPSDDICYATQNRQVAVKALAERCELMIVVGSRNSSNSVRLVEVAKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGHPEVEGTMGQYEKCTEGGGIYLVETPEDVRNLK--VNNPNDLAYVTQTTLSMTDTKVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EAPEGANMVFSAHGVSPMVHEBAAAKNIKAIDAACPLVTKVHKEVQRFDKQGFHILFIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KILLAAPRGYCAGVDRAVETVERALBEYGAPIYVRKEIVHNRYVVDTLAEKGAIFVNEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 AA;
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                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                   Protein; 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322
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Pred. No. 3.4e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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98
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine chemical production can be modulated. The presence of (1) or the SRT proteins (111) encoded by them are used for disgnosing the presence or activity of Corynebacterium diphtheriae. (1), (111), (111) and host cells containing them can be used to map the genomes of organisms related to C. glutamicum, to identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determination of SRT protein regions required for function, in modulating the SRT protein activity, and in modulating the activity of an SRT pathway. (11) are used to permit C. glutamicum to survive in an environment that is normally environmentally or chemically hazardous to it. (1) and protein molecules encoded by it increase the survivel of C. glutamicum to chemical and environmental hazards and provide a means for continued growth and environmental hazards show the fermentative growth conditions. By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JUL-1999;
08-JUL-1999;
09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF70984 to AAF71133 encode the Corynebacterium glutamicum stress, resistance, and tolerance (SRT) proteins given in AAB78871 to AAB79020. The C. glutamicum SRT genes (I) can be used in vectors (II) for expression in host cells and production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred organic acid, a proteinogenic or nonproteinogenic amino acid (preferred
                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  increasing the growth rate or maintaining a normal growth rate in poor toxic conditions, the yield, production and/or efficiency or production of fine chemicals from a culture may be increased.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; Page 249-250; 526pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated Corynebacterium glutamicum nucleic acid encoding a tolerance or resistance protein, for production or modulation of production of fine chemicals, such as, e.g. amino acids, lipids, carbohydrates, or enzymes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pompejus M,
Kim H;
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27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                    QIVLANPRGFCAGVDRAIEIVDQAIEAFGAPIYVRHEVVHNRTVVDGLKQKGAVFIEELS
                                                                                                                  AGHPEVEGTMGQYEKCTEGGGIYLVETPEDVRNLK--VNNPNDLAYVTQTTLSMTDTKVM 179
                                                                                                                                                                                         DVPVGSYLIFSAHGVSKEVQQEASERQLTVFDATCPLVTKVHMQVAKHAKQGREVILIGH 121
VRELKVKFPQLQDPPSDDICYATQNRQVAVKAIAERCELMIVVGSRNSSNSVRLVEVAKQ
                                 VDALREQFPSIKEQKKDDICYATQNRQDAVHDLAKISDLILVVGSPNSSNSNRLRBIAVQ
                                                                                                                                                       EAPEGANMVFSÄHGVSPMVHEEÄAAKNIKAIDÄACPLVTKVHKEVQRFDKQGFHILFIGH
                                                                                                                                                                                                                              KILLAAPRGYCAGVDRAVETVERALBEYGAPIYVRKEIVHNRYVVDTLAEKGAIFVNEAS
                                                                                                                                                                                                                                                                                                                                                                                325 AA;
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99DE-1031541.
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99DE-1032230.
99DE-1032214.
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99US-0151214.
99DB-1041382.
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-S066
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Pred.
                                                                            -HIVDGVAGIATLPEFLNDEPNL
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                                                                                                                                                                                                                                                                                                                       755; DB 22;
No. 3.4e-61;
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                                                                                                                                                                                                                                                                                                                                         Length 325;
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V----PVGSYLIFSAHGVSKEVQQEAEERQLTVFDATCFLVTKVHMQVAKHAKQGREVIL 118

VLLASPRSFCAGVERAIETVKRVLDVAEGPVYVRKQIVHNTVVVAELRDRGAVFVEDLDE IVLANPRGFCAGVDRAIBIVDQAIBAFGAPIYVRHEVVHNRTVVDGLKQKGAVFIBELSD

79

20

Matches Query Match Best Local (

150;

Conservative

60;

Indels

Gaps

(u)

Score 743.5; DB Pred. No. 4e-60; 0; Mismatches

BG 94, 22;

Length

329; 11;

Similarity

45.88;

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RESULT 9
AAG81220
ID AAG81220
ID AAG8
XX AAG8
XX AAG8
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                                                                                          polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polymucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of
       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 187; 207pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         involves providing between nucleotide
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                                                                        an organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to a method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA
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12-NOV-1999;
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       329 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth; organism viability; characterisation
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12-NOV-1999;
01-FEB-2000;
                                 method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of
                                                                                                                     This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polymucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The
                                                                                                                                                                                                                                                                Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
                                                                                                                                                                                                                         Disclosure; Page 165; 207pp; English.
                                                                                                                                                                                                                                                     sequences
                                                                                                                                                                                                                                                                                                                                                                   Eisenberg D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis
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Sequence

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organism.

AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX391990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, simusitis, purulent otitis media, crythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                             Griffais R;
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21-NOV-1997;
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                                                                                                                                                                                                                                      Page 1389; Disclosure; 1912pp; English.
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sinusitis; purulent o
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97FR-0014673.
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Pred. No. 3.8e-59;
6; Mismatches 92;
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Best Local Sim
Matches 143;
     Claim
                             New Chlamydia pneumoniae proteins or antigens, useful for the prophylactic or therapeutic treatment of Chlamydial bacterial infections, e.g. sinusitis, pharyngitis, bronchitis, or chronic obstructive pulmonary disease
                                                                                                                                                                                                                                                                                                                                                         CWL-029; BVF-CPN; antibiotic; antibacterial; Chlamydial infection; sinusitis; pharyngitis; bronchitis; pneumonitis; asthmatic bronchi adult-onset asthma; chronic obstructive pulmonary disease; COPD;
                                                                                                                                                                                                                                                                                                                                                                                                                 C. pneumoniae BVH-CPN18 from strain CWL-029.
                                                                                                                                                                                                                                                                                                                                                                                                                                              08-OCT-2002
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                                                                                                                                                                                                                                                                                                               Chlamydia pneumoniae.
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       9; Figure
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                                                                             08-MAY-2000;
30-MAY-2000;
16-JUN-2000;
16-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP binding cassette; secretary locus open reading frame; endopeptidase; secretary locus ORF; protease; metalloprotease; CLP protease ATPase; CLP protease subunit; transglycolase/transpeptidase; CLPc protease; thioredoxin; Chlamydia infection; antibacterial.
                       16-JUN-2000;
16-JUN-2000;
                                                                                                                                                                                                                 08-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QIVLANPRGECAGVDRAIEIVDQAIEAFGAPIYVRHEVVHNRTVVDGLKQKGAVFIEELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----EKVVESIPKELK 313
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; 2000US-207852P.
; 2000US-211796P.
; 2000US-211797P.
; 2000US-211798P.
; 2000US-211801P.
; 2000US-212044P.
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                                                                                                                                                                                                                                                                                                                                                                                   CWL029
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RESULT 14
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Best Local
Bifidobacterium longum NCC2705; Bifidobacterium; bacterial; antidiarrheic; antibacterial; inhibitor of Salmonella; dete identification; lactic acid bacterium; diarrhoea; pathogeni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the isolation of Chlamydophila pneumoniae strain CWLO29 genes and their encoded proteins. The genes the invention encode an ATP binding cassette gene, a secretary locus open reading frame (ORP), an endopeptidase, a protease, a metalloprotease, CLP protease ATPase, a CLP protease subunit, a transglycolase/transpeptidase, a CLP protease, or thioredoxin. The genes of the invention can be used in a vector as a vaccine for the prevention and treatment of Chlamydia infections. Also described are prevention and treatment of Chlamydia infections.
                                                           Bifidobacterium
                                                                                             19-NOV-2002
                                                                                                                           ABP66088
                                                                                                                                                       ABP66088 standard; Protein; 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine useful for immunising mammals against chlamydia infections, comprises vectors having sequences of ATP binding cassette gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-SEP-2000; 2000US-235335P
26-SEP-2000; 2000US-235361P
26-SEP-2000; 2000US-235398P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and T-cell epitopes from the proteins of the invention which can be ed as Chlamydia antigens. AAU09430-AAU09439 represent the proteins coded by the C. pneumoniae genes (AAS18750-AAS18759) of the invention
                                                                                                                                                                                                                                                                                                                                                               178
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                                                                                                                                                                                                                                    NDIFAVEDVVFQLPKELR 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGHPEVEGTMGQYEKCTEGGGIYLVETPEDVRNLKVNNPNDLAYVTQTTLSMTDTKVMVD
                                                                                                                                                                                                                                                                                                                                                                                         ALREQFPSIKEQKKDDICYATQNRQDAVHDLAKISDLILVVGSPNSSNSNRLREIAVQLG
                                                                                                                                                                                                                                                                                               VPADLINNPEDIDTNIVNHSGDIAMTAGASTPEDVVQACIRKL-----
                                                                                                                                                                                                                                                                                                                             KPAYLIDTYQDLKQDWLEGIEVVGVTAGASAPEVLVQEVIDQLKAWGGETTSVRENSGIE
                                                                                                                                                                                                                                                                                                                                                                                                                         KKHVEVIGIVGEVPE-----HITVVEKVADVBALPFSSDTPLFYITQTTLSLDDVQEISS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVPEGERVIYSAHGIPPSVRAEAKARKLIDIDATCGLVTKVHSAAKLYASKGYKIILIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLILCNPRGFCSGVVRAIQVVEVALEKWGAPIYVKHBIVHNRHVVNALRAKGAIFVEELV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QIVLANPRGFCAGVDRAIBIVDQAIBAFGAPIYVRHBVVHNRTVVDGLKQKGAVFIBBLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig 5; 35Spp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  locus open reading frame gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310
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                                                                                           (first
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                                                           longum NCC2705 ORF amino acid sequence
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                                                                                           entry)
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Pred. No. 9.9e-53;
9; Mismatches 98
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diarrhoea; pathogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 310;
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                detection;
                                                             SEQ
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 bacteria;
                                                             NO:832
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227

SSNSNRLREIAVQ-LGK--PAYLIDTYQDLKQDWLEGIEVVGVTAGASAPEVLVQEVIDQ

TQTTLSMTDTKVMVDALREQFPSIKEQKKDDICYATQNRQDAVHDLAKISDLILVVGSPN LRFVREGYEIVYIGHKGHDEAVGVVGESPE----HVHLIEHESDVDSLDFAPDTKLVLL AKHAKQGREVILIGHAGHPEVEGTMGQYEKCTEGGGIYLVETPEDVRNLKVKNPNDLAYV

SOTTLSVDETADTIAALKAKEPWIQEPPSSDICYATSNRQAAVKLVAQQSDCVVIVGSAN

261 226 201 166 146 106 8

202

167

147

107

87

52 KGAVFIEELSDVP-----VGSYLIFSAHGVSKEVQQEAEERQLTVFDATCPLVTKVHMQV

QGAVFVQELAEI PDAAAQAGI PVVFSAHGVSPVVKAEAERRGMHVVDATCPLVGKVHREV

3 IVLANPRGFCAGVDRAI---EIVDQAIEAFG-----APIYVRHEVVHNRTVVDGLKQ

VVLADPRGFCAGVDRAILTVQTILKAAEASGKRTREDGLPPVYVRRQIVHNKHVVEDLAG

27

Matches Query Match Best Local

145;

Conservative

64;

Similarity

40.5%;

Score 658; DB 23; Pred. No. 3.5e-52; Mismatches

Length 352; Indels

26;

Gaps

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CC The present invention describes a polynucleotide (I) comprising a CC sequences of a Bifidobacterium genome selected from the nucleotide CC sequences given in AB981842 and AB981843, or a sequence exhibiting at CC least 90% identity or which hybridises with the sequences given in CC AB981842 and AB981843. Also described is a polynucleotide (II) encoding CC affision protein, comprising a sequence selected from 1097 sequences GC given in AB98258 to ABP6354 ligated in frame to a polynucleotide (II) encoding a heterologous polypeptide. (I) has antidiarrheic and CC antibacterial activities, and can be used as an inhibitor of Salmonella. CC (I) (which is a probe) is useful for the detection and/or identification of Bifidobacterium longum in a biological sample. A carrier containing CC the lactic acid bacterium Bifidobacterium longum NCC2705 (CNCM I-2618) CC can be used for preventing and/or treating diarrhoea brought about by pathogenic bacteria and/or rotavirus. The carrier is a food composition concept from milk, yogurt, curd, cheese, fermented milks, milk based fermented products, incential, pet food or a pharmaceutical composition consposition selected from tablets, liquid bacterial suspensions, dried oral supplement, wet oral supplement, dry tube feeding or wet tube feeding. (I) is useful in DNA arrays or chips to carry out analysis of the Sidobacterium related mucleotide sequences given in the Sequence of the milks of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequenc
Sequence
                                                                             N.B. The sequence data for specification but is based
                                                                                                                                                            Listing from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotide comprising Bifidobacterium genome sequence useful as a probe or primer for detecting and/or identifying Bifidobacterium longum in a biological sample
                                                                                                                                   specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; SEQ ID 832; 80pp; English
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                                                      Patent Office.
352
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                                                                             chis patent
on sequence
                                                                                                                                                          sequences given in the Sequence but not mentioned further within the
                                                                             is not represented in the information supplied by the
                                                                             the printed
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RESULT 15
AAY37259
ID AAY377
XX AAY377
XX AAY37
XX AMAINO
XX AMAINO
XX VACCI
KW PARTAIT
KW NOO90
XX HOO90
XX HOO90
XX O1-JU
PF 27-NO
XX 04-NO
PF 27-NO
XX 04-NO
PF 17-DE
XX 04-NO
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Best Local Simi
Matches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention
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28-NOV-1997;
17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome sequence of Chlamydia trachomatis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          may be of use in treating these diseases.
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Pred. No. 3.5e-52;
3; Mismatches 100;
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EMDLFVEEDTVFQLPKEL 307
                                   RENSGIBEKVVFSIPKEL 312
                                                                          VTARLVNHPDEVTEEILQYSGNIGITAGASTPEDVVQACLMKLQELIPDL-----SI
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Search completed: January 29, 2004, 15:49:46
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Result
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

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1348.130 Million cell updates/sec
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Sequence 6046, Ap
Sequence 429, App
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29 121 HAGHPEVBGTMGQYEKCTEGGGIYLVETPEDVRNIKVNNPNDLAYVTQTTLSMTDTKVMV 180	Query Match 64.6%; Score 1048.5; DB 4; Length 336; Best Local Similarity 64.2%; Pred. No. 2.5e-98; Matches 203; Conservative 49; Mismatches 61; Indels 3; Gaps 2; 2y 1 MQIVLANPRGFCAGUDRAIELVDQAIEAFGAPIYVRHEVVHNTTVDGLKQKGAVFIBEL 60	RESULT 1 US-09-328-352-6046 ; Sequence 6046, Application US/09328352 ; Patent NO. 6562958 ; GENERAL INFORMATION: APPLICANT: Gary L. Breton et al. TITLE OF INVENTION: BUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC99-03PA CURRENT APPLICATION NUMBER: US/09/328,352 CURRENT FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 8252 ; SEQ ID NO 6046 LENGTH: 336 TYPE: PRT CURGANISM: Acinetobacter baumannii US-09-328-352-6046	28 93 5.7 573 5 PCT-US96-11375-1 29 93 5.7 981 4 US-09-252-991A-18616 Sequence 1, Appli 30 91.5 5.6 298 3 US-08-961-083-24 31 91.5 5.6 298 4 US-09-172-422-1 32 91.5 5.6 2548 4 US-09-172-422-1 33 91 5.6 335 4 US-09-34-901-6 34 90.5 5.6 540 4 US-08-34-303-251-3 35 90.5 5.6 540 4 US-08-34-251-3 36 90.5 5.6 540 4 US-08-346-241-3 38 90.5 5.6 540 4 US-08-362-3 39 90.5 5.6 541 2 US-08-467-822-34 Sequence 3, Appli 39 90.5 5.6 541 2 US-08-447-154-19 40 90.5 5.6 541 3 US-08-447-154-19 41 90.5 5.6 541 3 US-08-42-6697-34 42 90.5 5.6 541 3 US-08-42-6697-34 43 88.5 5.5 885 3 US-08-841-089-2 ALIGNMENTS ALIGNMENTS
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RESULT 2 US-09-199-637A-429 ; Sequence 429, Application US/09199637A

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PRIOR APPLICATION NUMBER: 60/066,517;
PRIOR FILLING DATE: 1997-11-25;
NUMBER OF SEQ ID NOS: 437;
SOFTWARE: FRACESEQ for Windows Version '
SEQ ID NO 429;
PRIOR THE 1349
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-429
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,768
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21399
LENGTH: 368
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, Sequence 21399, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
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TITLE OF INVENTION: VIRILENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
                                                                                                                                                                             TITLE OF INVENTION: NUCLEIC TITLE OF INVENTION: AERUGIN FILE REFERENCE: 107196.136
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                                                                                                                                                                                             Marc J. Rubenfield et al.

VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
VENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Mahajan-Miklos, Shalina
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63.3%; Pred. No. 2.96
ative 49; Mismatches
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US-09-198-452A-1090
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US-09-252-991A-21399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1090
LENGTH: 310
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Griffals, R.
APPLICANT: HILLS OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment:
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preventing of INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1090, Application US/0919B452A
Patent No. 6559294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 198; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                         ttch 40.9%; Score 663; DB 4; Length 310; cal Similarity 45.0%; Pred. No. 3.7e-59; 143; Conservative 59; Mismatches 98; Indels
                                         178
242 KPAYLIDTYQDLKQDWLEGIEVVGVTAGASAPEVLVQEVIDQLKAWGGETTSVRENSGIE 301
                                                                                                                               123 KKHVEVIGIVGEVPE-----HÍTVVEKVADVEALPFSSDTPLFYITQTTLSLDDVQEISS 177
                                                                                                                                                                      122 AGHPEVEGTMGQYEKCTEGGGIYLVETPEDVRNLKVNNPNDLAYVTQTTLSMTDTKVMVD 181
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                                                                                                                                                                                                                  DVPEGERVIYSAHGIPPSVRAEAKARKLIDIDATCGLVTKVHSAAKLYASKGYKIILIGH
                                                                                                                                                                                                                                                          DVPVGSYLIFSAHGVSKEVQQEASERQLTVFDATCPLVTKVHMQVAKHAKQGREVILIGH 121
                                                                                                                                                                                                                                                                                                      KLILCNPRGFCSGVVRAIQVVEVALEKWGAPIYVKHEIVHNRHVVNALRAKGAIFVEELV 62
                                         ALLKRYPSIITLPSSSICYATTNRQKALRSVLSRVNYVYVVGDVNSSNSNRLREVALRRG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDVPVGSYLIFSAHGVSKEVQQEAEERQLTVFDATCPLVTKVHMQVAKHAKQGREVILIG
                                                                              ALREOFPSIKEOKKODICYATONRODAVHDLAKISDLILVVGSPNSSNSNRLREIAVOLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BEKVVFSIPKELK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTPAYLIDGAEDMQRGWFDGVRRIGITAGASAPEVLVRGVIAQLREWG--ASEEQELBGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKPAYLIDTYQDLKQDWLEGIEVVGVTAGASAPEVLVQEVIDQLKAWGGETTSVRENSGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DALREGEPSIKEGKKODICYATGNRQDAVHDLAKISDLILVVGSPNSSNSNRLREIAVQE
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63.3%; Pred. No. 3.2e-96;
tive 49; Mismatches 63
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US-09-107-532A-6431
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                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...521
SEQUENCE DESCRIPTION: SEQ ID NO: 6431:
US-09-107-532A-6431
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: LYNN A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                      Query Match
Best Local S
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NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/107,532A
PILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
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MEDIUM TYPE: CD/ROM ISO9660
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                                                                                                                                                                112 EVVDHTSLVEGNEMKIDSFIAELGOPSMDLYVYDLDENLIFKTHENSRNLIQTTRK---- 167
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                                                                                                                        91 VFDATCPLVTKVHMQVAKHAKQGREVILIGHAGHPEVEG--TMGQYEKCTEGGGIYLVET 148
                                                                                                                                                                                                        38 EVVHNRTVVDGLKQKGAVFIEELSDVPVGSY-----LIFSAHGVSKEVQQEAEERQLT
                                                                                                                                                                                                                                                      63;
                                                                                                                                                                                                                                                    Similarity 20.9
63; Conservative
FYDIRNKLL-----LTLIVLEVVSLILSSILGFFLSSYFLKPLKVLRDTMDTIRKDPQSD
                                   PEDVRNIKVNNPNDLAYVTQTTISMTDTKVM-----VDALREQFPSIKEQKKDD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 521 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (781)893-50
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Waltham
STATE: Massachusetts
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                                                                                                                                                                                                                                             7.2%; Score 116.5; DB 4; Length: 20.9%; Pred. No. 0.0035; tive: 52; Mismatches 104; Indels
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                                                                                VTLEGKTGFLSIQPIYSKGTREKIGYAQSFYELSS
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                        DB 4; Length 521;
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US-08-198-446B-19

Sequence 19, Application US/08198446B Patent No. 5674996 GENERAL INFORMATION:

APPLICANT: APPLICANT:

Hartwell, Lelan Weinert, Ted A. Plon, Sharon E.

Leland H.

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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILLING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5024
LENGTH: 494
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LYNN DOUGETTE-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: GTC-007
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  308
                                         289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 KGAVFIEELSDVPVGSYLIFSAHGVSKEVQQEAEERQLTVFDATCPLVTKVHMQVAKHAK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
GPGSICTTRVVAGVGVPQITAVYDCATEARKHGKA
                                                                                AGVDALIIDTAHGHSKGVINQVKHIKETYPEITVVAGNVATAEATRALFEAGADVVKVGI 307
                                                                                                                    LGKPAYLIDT-----YQDLKQDWLEGIEVVGVTAGASAPEVLVQEVIDQLKAWG 288
                                                                                                                                                                KIEKLPLVENGRLEGLITIKDIEKVLEFPYAAKDEHGRLLAAAAIGTSKDTEIRAQKLVE
                                                                                                                                                                                                  KKDDICYATONROD---AVHDLAKISDL------ILVVGSPNSSNSNRLR-EIAVQ 239
                                                                                                                                                                                                                                                                                     GIYLVETPEOVRNLKVNNPNDLAYVTQTTLSMTD----TKVMVDALREQFPSIKEQ 193
                                                                                                                                                                                                                                                                                                                              QGGLGVIHKNMGVEEQADEVQKVKRSENGVISNPFFLTPBESVYEABALMGKYRI----S 127
                                                                                                                                                                                                                                                                                                                                                                     QGREVILIGHAG-----
                                      GE----TTSVRENSGIEE-KVVFSIPKELKKHMQA 318
                                                                                                                                                                                                                                                GVPIVDNQEDRKLIGILTNRDLRFIEDFSIKISDVMTKDNLITAPVGTTLDEABAILQKH 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.4%; Score 104; DB 4; Length 494; ilarity 19.1%; Pred. No. 0.06; Conservative 63; Mismatches 134; Indels
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RESULT 8
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                                                                     Sequence 19, Application US/08870693
Patent No. 5866338
GENERAL INFORMATION:
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIA RE-lease #1.0, V.
CURRENT APPLICATION DATA:
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                                  APPLICANT:
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DESCRIPTION:
 APPLICANT:
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LENGTH: 586 amino aci
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ADDRESSEE: Christens
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TITLE OF INVENTION: Cell Cycle Checkpoint
NUMBER OF SEQUENCES: 19
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FILING DATE: 18-FEB-1994
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                    GHVDFRGEVSRSYASC--GGAILLVDASQGIQAQTVAN-FYLAFSLGLKLIPVINKIDLN 179
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1420 Fifth Ave., Suite 2800
               Hartwell, Lel
Weinert, Ted
Plon, Sharon
Groudine, Mark T.
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yeast MEC3 protein
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                                                    Leland H.
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: prote
; DESCRIPTION: yeast
US-08-870-693-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: May 12, 1993
APPLICATION NUMBER: US 07/
FILING DATE: May 14, 1992
APPLICATION NUMBER: US 07/
FILING DATE: May 12, 1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                               123 GHVDFRGEVSRSYASC--GGAILLVDASQGIQAQTVAN-FYLAFSLGLKLIPVINKIDLN
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Similarity 21.9%;
                                                                                                                                                                                                                   SNRLREIAVQLGKP--AYLIDTYQDLKQDWLEGIEVVGVTAGASAPEVLVQEVIDQLKAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THVIDENARNKQVLDKLEVERERGITIKAQTCSM-----FYKDKRTGKNYLLHLIDTP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----KEVQQEAE---ERQLTVFDATCPLVTKVHMQVAKHAKQGREVI--LIGHA 122
                                                                     GGETTSVRENSGIBEKVVPSIPKE 311
                                                                                                                                                                                                                                                                                        FTDVKQVKDQIVNNF----ELPEEDIIGVSRKTALNVEELLLPAIIDRIPPPTGRPD---
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206-224-0779
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--VRKN----DKVICAQTKE 274
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тимвек: US 07/882,051
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US-08-467-822-35
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; LENGTH: 540
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-134-001C-4705
                                                                                                                                                                                                                                                                                                                                                           Sequence 35, Application US/08467822 Patent No. 5843460
                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4705, Application US/09134001C Patent No. 6380370
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PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION STAPPLICATION NUMBER: US/09/134,001C
                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   APPLICANT:
                        NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSE: Finnegan, Henderson,
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
                                                                                                                                        APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 DASLDML--GTANKVEVTKOHTTVVD-----GNGDENNIDARVGQIKAQIEETDSEFDKE 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANPRGFCAGVDRAIEIVDQAIEAFGAPIYVRHEVVHNRTV-------VDGLKQ 51
                                                                                                                                                                                                                                                                                                          Labigne, Agnes
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                                                                          Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----NDLAYVTQTTLSMTDTKVMVDALREQFPSIK 191
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US-08-432-697-35
; Sequence 35, Application US/08432697
; Patent No. 6248330
                                                                     RESULT 11
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COMPUTER READABLE FORM:

MEBIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARB: Patentin Release #1.0, Version #1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,822

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
FILING DATE: 02-MAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 YEKCTEGGGIY----LVETPEDVRNLKVNNPNDLAYVTQTTLSMTDTKVMVD-----ALR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 QSIVPALEIANLVLNRLKVGLQVVAVKAPGFLVLNRLKVGLQVVAVKAPGFGDNRKNQLK 289
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 547 amino acids
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity es 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meyers, Kenneth J. REGISTRATION NUMBER: 25, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0
FILING DATE: 02-MAY-1995
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STREET: 1300 I Street, N.W.
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                                                                                                                     344 KRIQEIIEQL--DVTTSEYEKEKLNERLAKLSDGVAVLKVGGTSDVEVNEKKDRVTDALN 401
                                                                                                                                                        185
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                283 QLKAWGGETTSVRENSGIEEKVVFSIPKELKKHMQA 318
                                                 402 ATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIIKRTLKIPA-
                                                                                                                                                                                                                         134 YEKCTEGGGIY----LVETPEDVRNLKVNNPNDLAYVTQTTLSMTDTKVMVD-----ALR 184
                                                                                                                                                                                                                                                                                                                            170 RKGVITVKDGKTLNDELEIIEGMKFDRGYISPÝFINTSKGQKCEFQDAYVLLSEKKISSI 229
                                                                                                                                                                                                                                                                                               93
                                                                                                                                                                                                                                                                                                                                                              51 QKGAVFI------EELSDVP-----VGSYLIFSAHGVSKEVQQE---AEERQLTVF 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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Ferrero, Richard L.
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                                                                                  -BIAVQLGKPAYL-----IDTYQDLKQDWLEGIEVVGVTAGASAPEVLVQEVID 282
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HELICOBACTER INFECTION, POLYPEPTIDES FOR
COMPOSITIONS, AND NUCLEIC ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Agnes
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                                                                                                                                                                                                                                                                                             --TKVHMQVA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 101; DB 3
Pred. No. 0.14;
65; Mismatches 1
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                                                                                                                                                                                        PHDLGKVGEVIVTKDDAMLLKGKGDKAQIE 343
                                                                                                                                                                                                                                                                                             ---KHAKQGREVILIGHAGHPEVEGTMGQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143;
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US-08-466-248-35
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                                                                                                                                                                                         Matches
                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
PRILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
PILING DATE: 02-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                             170 RKGVITVKDGKTLNDELEIIEGMKFDRGYISPYFINTSKGQKCEPQDAYVLLSBKKISSI 229
230 QSIVPALEIANLVLMRLKÝGLÓVVAVKAPGFLVLMRLKVGLOVVAVKAPGFGDNRKNOLK 289
                                                                                                                          110 ANPVBIRRGVDLAVDAVIAELKKQSKPVTTPBEIAQVATISANGDKBIGNIISDAMKKVG
                            93 DATCPLV-----TKVHMQVA------KHAKQGREVILIGHAGHPEVEGTMGQ 133
                                                                                           51 QKGAVFI-----BELSDVP------VGSYLIFSAHGVSKEVQQB---AEERQLTVF
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linear
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Ferrero, Richard L.
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                                                                                                                                                                                                     6.2%; Score 101; DB 3; Length 547; 18.2%; Pred. No. 0.14;
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POLYPEPTIDES
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                                                                                                                                                                                         Mismatches 143;
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US-08-144-121-4
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CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/144,121
FILING DATE: 27-0CT-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 36,965
REFERENCE/DOCKET NUMBER: 0,000 MGP-021
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
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                                                                                                                                                                                                                                                                                                                                                                                                            TBLEFAX: (617) 227-594
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Burgeson, Robert E.
APPLICANT: Wagman, David W.
TITLE OF INVENTION: B1k CHAIN OF LAMININ AND METHODS OF
                                                           LOCATION: FEATURE:
                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide FRAGMENT TYPE: internal
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CORRESPONDENCE ADDRESS:
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STREET:
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                                         NAME/KEY:
                                                                                                 NAME/KEY:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
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ZIP: 02109
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60 State Street, suite 510
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US-08-735-893-4
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Best Local Similarity 19.8%;
Matches 52; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Burgeson, Robert E.
APPLICANT: Wagman, David W.
TITLE OF INVENTION: BIK CHAIN OF LAMININ AND METHODS OF USE
NUMBER OF SEQUENCES: 14
                                                                                                                                                                     TELEFAX: (617) 227-594
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                        MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: (MITTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/144,121
FILING DATE: 27-OCT-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suit
FEATURE:
                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                    LOCATION:
                                       NAME/KEY:
                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/735,893
                                                                                                                                                    BNGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 LIFSAHGV---SKEVQQE-----AEERQLTVFDATCPLVTKVHMQVAKHAKQGREVILIG 120
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                                                                                                                                                        1196 amino acids
                                                                                                                                                                                                              (617) 227-74
(617) 227-5941
                  Domain
1..250
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                                                                              peptide internal
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US-08-797-358B-3
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US-08-735-893-4
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Best Local &
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INFORMATION FOR SEQ ID NO: 3:
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NAME/KEY:
                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/797,358B
FILING DATE: 11-Feb-1997
CLASSIFICATION NUMBER: US 60/011,491
PRIOR APPLICATION NUMBER: US 60/011,491
FILING DATB: 12-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REFERRNCE/DOCKET NUMBER: 9-CE 3165
REFERRNCE/DOCKET NUMBER: 9-CE 3165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
FEATURE:
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                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1044 TAASEETLENASQRISELERNVE 1066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         989 KRASKSATDVKVTADMVKEALEBAEKAQVAA-----EKAIKQADEDIQGTQNLLTSIESE 1043
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52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----KTNATKEKMDK-----SNEELRNLIKQIRN----FLTQDSADLDSIEA 933
              TELEFHONE: (619) 535-9001
TELEFAX: (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EE: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.88;
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Pred. No. 0.71;
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
375
                                                                               335 DVVLVGGSTR-
                                                                                                                                                                                                     169 TILSMIDIKVMVDALREQ---PPSIKEQKKDDICY-----ATQNRQDAVHDLAKIS 216
                                                                                                                                                                                                                                                                                       132 GQYEKCTEGGGIYLVETPEDVRNLKVN------NPNDLAY------VTQ 168
                                                                                                                                                                                                                                                                                                                                 186 GLDR----RGAGERNVLIFDLGGGTFDV----
                                                                                                                                                                                                                                                                                                                                                                                                                  131 BTAEAYLGQP--VKHAVITVPAYFNDSQRQATKDAGAIVGLNVLRIINEPTAAAI---AH
                                                                                                                                                                                                                                                                                                                                                                          75
                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 QAIEAF-GAPIYVRHEVV-----HNRTVVDGLKQKGAVF---IEELSDVPVGSYLIFSAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
AAVQAAVLMGDKCEKVRDLLLLDVAPLSLGLETAGGVMTTLIQRNATIPTK 425
                                                                                                                      DLILVVGSPNSSNSNRLREIAVQLGKPAYLIDTYQDLKQDWLEGIEV-----VGVTAG
                                                                                                                                                                                                                                                 GD----THLGG-----BDFDNRLVNHFVEEFRRKHRKDLSWNKRALRRLRTACERAKR
                                                                                                                                                                                                                                                                                                                                                                        GVSKEVQQEABERQLTVFD---ATCPLVTKVHMQVAKHAKQGREVILIGHAGHPEVEGTM 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 643 amino acids TYPE: amino acid
                                     ASAPEVLV-----QEVIDQL------KAWGGETTSVRENSGIBEK 303
                                                                                                                                                              TLSSSTQATLEIDSLFEGVDFYTSITRARFEELCSDLFRSTLEPVBKGLRDAKLDKAXIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.9%; Score 95.5; DB 3; 21.9%; Pred. No. 0.67;
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                                                                                 IPRVQKLLQDPFNGKBLNKSINPDEAVAYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102;
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18;

Search completed: January 29, 2004, 15:57:09 Job time: 11.9804 secs

269 334

Copyright

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                           663
663
598.5
111
109
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US00C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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length: 2000000000
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1623
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    789580 segs, 207824079 residues
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US-09-934-903-24
US-09-941-947A-18
US-09-975-719-429
US-10-156-761-10747
US-09-738-626-4643
US-09-712-363-188
US-10-289-762-1090
US-10-289-762-1090
US-10-275-360-5
US-10-156-761-10047
US-09-712-363-282
US-10-369-493-19263
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                                                                                                                                                                                                                                                                                                               Description
                                      Sequence 24, Appl
Sequence 18, Appl
Sequence 429, App
Sequence 10747, A
Sequence 271, App
Sequence 271, App
Sequence 1090, App
Sequence 36, Appl
Sequence 5, Appli
Sequence 10047, A
Sequence 282, App
Sequence 3815, Ap
Sequence 5415, Ap
                      Sequence
Sequence
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ALIGNMENTS

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SOFTWARE: Microsoft Office 97
SEQ ID NO 24
LENGTH: 318
TYPE: PRT
ORGANISM: Methylomonas 16a
US-09-934-903-24
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                                                                                                                                      Query Match
Best Local Similarity
Matches 318; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                        APPLICANT: Picataggio, Stephen
APPLICANT: Cheng, Qiong
TITLE OF INVENTION: Genes Involved in Isoprenoid Compounds Production
FILE REFERENCE: CL1646 US NA
CURRENT APPLICATION NUMBER: US/09/934,903
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR PILING DATE: September 1, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KOffas, Mattheos
APPLICANT: Odom, J. Martin
APPLICANT: Schenzle, Andreas J.
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
 61
                      61 SDVPVGSYLIFSAHGVSKEVQQEAEBRQLTVFDATCPLVTKVHMQVAKHAKQGREVILIG
                                                                   SDVPVGSYLIFSAHGVSKEVQQEASERQLTVFDATCPLVTKVHWQVAKHAKQGREVILIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tomb, Jean-Francois
Rouviere, Pierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. US20020102690Alton,
                                                                                                                                  100.0%; Score 1623; DB 10; ilarity 100.0%; Pred. No. 2.5e-150; Conservative 0; Mismatches 0;
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                                                                                                                                        Indels
                                                                                                                                                                      Length 318;
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RESULT 2
US-09-941-947A-18
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LENGTH: 318
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Publication No.
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APPLICANT:
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CURRENT FILING DATE: 2001-09-01
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Brzostowicz, Patricia C. APPLICANT: Cheng, Qiong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Picataggio, Steve
APPLICANT: Rouviere, Pierre E.
TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE
FILE REFERENCE: CL1903 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Methylomonas 16a
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EEKVVFSIPKELKKHMQA 318
                                                                                                                                                DALREQFPSIKEQKKDDICYATQNRQDAVHDLAKISDLILVVGSPNSSNSNRLREIAVQL
                                                                                                                                                                                                                                                       HACHPEVEGTMGQYEKCTEGGGIYLVETPEDVRNLKVNNPNDLAVVTQTTLSMTDTKVMV 180
                                                                 GKPAYLIDTYQDLKQDWLEGIEVVGVTAGASAPEVLVQEVIDQLKAWGGETTSVRENSGI
                                                                                           GKPAYLIDTYQDLKQDWLEGIEVVGVTAGASAPEVLVQEVIDQLKAWGGETTSVRENSGI
                                                                                                                                                                                     DALREOFPSIKEOKKODICYATONRODAVHDLAKISDLILVVGSPNSSNSNRLREIAVOL 240
                                                                                                                                                                                                                                                                                                              SDVPVGSYLIFSAHGVSKEVQQEASERQLTVFDATCPLVTKVHMQVAKHAKQGREVILIG 120
                                                                                                                                                                                                                                                                                                                                          SDVPVGSYLIFSAHGVSKEVQQEAEERQLTVFDATCPLVTKVHMQVAKHAKQGREVILIG 120
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Miller, Edward S
Odom, J. Martin
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DiCosimo, Deana J.
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No. US20030003528A1
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APPLICANT: Rabme, Laurence G.
APPLICANT: Rabme, Laurence G.
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 007086/351003
CURRENT APPLICATION NUMBER: US/09/975,719
CURRENT APPLICATION NUMBER: US 09/199,637
PRIOR FILING DATE: 1998-11-25
PRIOR FILING DATE: 1998-11-25
PRIOR FILING DATE: 1997-11-25
INDMESE OF SEQ ID NOS: 437
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 429
LENGTH: 349
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-975-719-429
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHERA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: KOYDEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
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                                                                                                                                                                                                                                                Sequence 10747, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    301
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o. US20030022349A1
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                                                                                                                                         FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILLING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR PELING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR PELING DATE: 2000-04-07
PRIOR FILLING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILLING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VEY: 3.0
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LENGTH: 338
  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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                                                      LENGTH: 325
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ~KPAYLIDTYQDLKQDWLEGIEVVGVTAGASAPEVLVQEVIDQLKAWGGETTSVRENSGI 300
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OZAKI, AKIO
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TATEISHI, NAOKO
SENOH, AKIHIRO
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  46.58;
Score
  755;
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                                                                                                                                             ; LENGTH: 329
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-271
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US-09-712-363-271
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CURRENT FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
PRIOR PPLICATION NUMBER: 60/179,531
PRIOR PPLICATION NUMBER: 60/117,844
PRIOR PPLICATION NUMBER: 60/117,844
PRIOR PILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/118,206,
PRIOR PILING DATE: 1999-02-01
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                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 292
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 271
LENGTH: 329
                                                               Matches 150;
                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY C
FILE REFERENCE: 07419-032001
CURRENT APPLICATION WITHOUT
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                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/165,086
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/134,092
PRIOR FILING DATE: 1999-05-14
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APPLICANT: Rotstein, Sergi
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/165,124
                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/126,593 FILING DATE: 1999-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/134,093
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2 QIVLANPRGFCAGVDRAIBIVDQAIBAFGAPIYVRHEVVHNRTVVDGLKQKGAVFIEBLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGHEEVEGTMGHSVEKT-----HLVDGVAGIATLPEFLNDEPNLIWLSQTTLSVDETMEI 189
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                                                            Conservative
                                                                                                                                                                                                                                                                                        1999-11-12
                                                                              45.8%; Score 743.5;
47.6%; Pred. No. 3.4
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7; Mismatches 86;
                                                               Mismatches
                                                                                  .4e-64;
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PRIOR PILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR PILING DATE: 2000-02-01
PRIOR PILING DATE: 2000-02-01
PRIOR PILING DATE: 1999-01-29
PRIOR PILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/118,206,
PRIOR PILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: 60/126,593
PRIOR PILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR PILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/134,092
PRIOR PILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/165,124
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR APPLICATION NUMBER: 60/165,086
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PRIOR APPLICATION NUMBER: 60/165,086
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR PILING DATE: 1999-11-12
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US-09-712-363-188
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                                                                                                                                                                          Matches
                                                                                                                                                                                              Query Match
Best Local
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Patent No. US20020164588A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Mycobacterium tuberculosis -09-712-363-188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                          socal Similarity
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                                  DVPVGSYLIFSAHGVSKEVQQEAEERQLTVFDATCPLVTKVHMQVAKHAKQGREVILIGH 121
                                                                                                             QIVLANDRGFCAGVDRAIEIVDQAIEAFGAPIYVRHEVVHNRTVVDG1KQKGAVPIBELS
QVPEGAIVVFSAHGVAPTVHVSASERNLQVIDATCPLVTKVHNEARRFARDDYDILLIGH
                                                                                   RVLLAEPRGYCAGVDRAVETVERALQKHGPPVYVRHEIVHNRHVVDTLAKAGAVFVBETE
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                                                                                                                                                                          Conservative
                                                                                                                                                                                          47.0%;
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                                                                                                                                                                       Score 733; DB 10;
Pred. No. 3.8e-63;
6; Mismatches 92;
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; NUMBER OF SEQ ID NOS: 6; SEQ ID NO 1090
; LEGHT : 310
; TYPE: PRT
; ORGANISM: Chlamydia pn
US-10-289-762-1090
RESULT 9
US-10-022-832-36
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US-10-289-762-1090
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Best Local :
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CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-27
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Sequence 36, Application US/10022832
Publication Wo. US20030059896A1
GENERAL INFORMATION:
APPLICANT: COUTURE, FRANCE
APPLICANT: HAMEL, JOSEE

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PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 28
SOPTWARE: Patentin version 3.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/10275360 Publication No. US20030115634A1 GENERAL INFORMATION:
                                 Matches
                                                                 Query Match
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Best Local Similarity
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SEQ ID NO 36
                                                                                                                                                                                                                                              TITLE OF INVENTION: GENES OF THE 1-DESOXY-D-XYLULOSE BIOSYNTHESIS PATH FILE REFERENCE: JOMAA-12 (PCT)
CURRENT APPLICATION NUMBER: US/10/275,360
CURRENT FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: PCT/EP01/04537
PRIOR FILING DATE: 2001-04-21
PRIOR FILING DATE: 2001-04-21
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CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/256,941
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 77
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                                                                                                              LENGTH: 539
TYPE: PRT
ORGANISM: Plasmodium
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TITLE OF INVENTION: NOVEL CHLAMYDIA ANTIGENS AND CORRESPONDING DNA
TITLE OF INVENTION: FRACMENTS
FILE REFERENCE: BIOVAC-15
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ORGANISM: Chlamydia
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3 IVLANPRGFCAGVDRAIEIVDQAIEAFGAPIYVRHEVVHNRTVVDGLKQKGAVFIEELSD 62
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45.0%; Pred. No. 2.4e-56;
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                                                36.9%;
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7
                                            Score 598.5; DB 1
Pred. No. 1.2e-49;
                                Mismatches
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; ORGANISM: Streptomyces avermitilis
US-10-156-761-10047
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US-10-156-761-10047
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PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 10047
LENGTH: 917
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Best Local Similarity
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
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APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIR
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250 YQDLKQDWLEGIEVVGVTAGASAPEVLVQ 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 LYLINDRGFCKGVSRAIETVEECLKLFKPPIYVKHKIVHNDIVCKKLEKEGAIFIEDLND 285
                                                                                                                                                                                                                                                                                                                                                                                                                      61 SDVPVGSYLIFSAHGVSKEVQQEAEERQLTVFDATCPLVTKVH--MQVAKHAKQGREVIL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  £83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 VLANPRGFCAGVDRAIBIVD----QAIBAFGAPIYVRHBVVHNRTVVDGLKQKGAVFIBEL
                                                                                                    KDDICYATQNRQDAVHDLAKISDLI-----LVVGSPNSSNSNRLREIAVQLGKPAYLIDT 249
                                                    RDDVTVGTKQKKBIDEDIGDDLDLLCQAAELVVSTQFGSTSMLQRKLRVGFAKAGRLMDL
                                                                                                                                                           LADSRVILDQPGAEKLIGKGDGLFLPMGANKPTRMQGAFVTEDEVEAVVQHCKDQMAPVF
                                                                                                                                                                                                                                                                ----DVBDAIVRITQLARAAGIHLVLATQRPSVDVVTGLIKANVPSRLAFATS---S
                                                                                                                                                                                                                                                                                                               IGHAGHPEVEGTMGQYEKCTEGGGIYLV---ETPE-DVRN--LKVNNENDLAYVTQTTLS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GHPEVEGTMGQYEKCTEGGGIYLVETPEDVRNIKVNNPNDLAYVTQTTLSMTDTKVMVDA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VPVGSYLIFSAHGVSKEVQQEABERQLTVFDATCPLVTKVHMQVAKHAKQGREVILIGHA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKNKFPHIETIPSGSICYATTNRQTALNKICTKCDLTIVVGSSSSSNAKKLVYSSQIRNV 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAYLIDTYQDLKQDWLEGIEVVGVTAGASAPEVLVQEVIDQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISHIKAWA, JUN
HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 111; DB 15; Length 917; Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                       ERELSPYPYLLVIVDELADLMMVAPR-----
                                                                                                                                                                                                              ---ALREQFPSIKEQK------
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SOFTWARE: FastSEQ for
SEQ ID NO 282
LENGTH: 578
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PRIOR APPLICATION NUMBER: 60/126,593
PRIOR FILING DATE: 1999-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/118,206,
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CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: INTERACTIONS OF PROTEINS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Eisenberg, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 6.7%;
Local Similarity 20.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/134,093
FILING DATE: 1999-05-14
APPLICATION NUMBER: 60/134,092
FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/179,531 FILING DATE: 2000-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/165,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/165,124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78;
                                        GGETTSVRENSGIEEKVVFSIP 309
                                                                            DRMREQAARIGRAT--LTRYAEVVQAGL
                                                                                                                  NRLRBIAVQLGKPAYLIDTYQDLKQDWLBGIEVVGVTAGASAPBVLVQEVIDQL---KAW 287
                                                                                                                                                                                                SIKEQKKDDICYATQNRQDAVHD-----LAKISDLILVVGSPNSSNS-----
                                                                                                                                                                                                                                      -IRAGGG----SPRDTLSVLDQLLAGAAD-THVTYTRALGLLGVTDVALIDDAV----D 254
                                                                                                                                                                                                                                                                              KCTEGGGIYLVETPED---VRNLKVNNPNDLAYVTQT----TLSMTDTKVMVDALREQPP 188
                                                                                                                                                                                                                                                                                                                     TEPEKVLPTIRSRTHHYPFRLLPPRTMRALLARICEQ--EGVVVDDAVYPLV------ 205
                                                                                                                                                                                                                                                                                                                                                               TCP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANDCGVCESCVSLAPNAPGSIDVVELDAASHGGVDDTRELRDR---AFYADVQSRYRV-- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANPRGFC-----
DAESALLQRVERIETRLDMSIP 388
                                                                                                                                                          ALAACDAAALFGAIESVIDGGHDPRRFATDLLERFRDLIVLQSVPDAASRGVVDAPEDAL 314
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20020164588A1
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                                                                                                                                                                                                                                                                                                                                                                                                   -----FIVDEAHMVTTAGFNALLKIVEEPPEHLIFIFAT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----AGVDRAIEIVDQAIEAFGAPIYVRHEVVH 41
                                                                                                                                                                                                                                                                                                                                                           --MQVAKHAKQGREVILIGHAGHPEVEGTMGQYE 135
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                                                                                --GEMRGATAPRILLEVVCARILLPSAS 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 578;
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROSIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-10-369-493-1052
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US-10-369-493-5415
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GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
FILE REFERENCE: 38-10(52052)B
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION UNMBER: US/0360,039
PRIOR APPLICATION UNMBER: US/0360,039
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SEQ ID NO 5415
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                                                                                                                                                                                                                                                                                                                                                              Sequence 1052, Application US/10369493 Publication No. US20030233675A1
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     NUMBER OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 DGTAAAL---SHGIFRRKEIGEKPORLMYYDMGAAKTTATIVEFKLVKEKYEKOPKMTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 MILANAKKFTEEYAQAAEIKOVVIT---VPVYF---TPAERLAVERAAQMAGLTVLQLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 GVG-----FDRTLGGIE-MTNRLRDHLIEMFE--KNYKPKTKVNTNRRA-MTKFSKEAE 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 VPVGSYLIFSAHGVSKEVQQEABERQLTVFD----ATCPLVTKVHMQVAKHAKQGREVIL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 IVLANPRGFCAGVDRAIEIVDQAIEAFGAPIYVRHEVVHNRTVVDGLKQKGAVFIEELSD 62
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SEQ ID NOS: 47374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLKQVLSANAEHFAQIESAHEDIDAKLKVTREDFNH---LISDMESRFGEP-IEQALRMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEAVAMGALFQAAHLSKGFKVKPFNIEEKVIFPV 434
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US-10-369-493-19263
; Sequence 19263, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT; ORGANISM: Myxococcus xanthus US-10-369-493-19263
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; LENGTH: 501
; TYPE: PRT
; ORGANISM: Methanococcus jannaschii
US-10-369-493-1052
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SLATER, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILLING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 19263
LENGTH: 1130
                                                                                                                                                                                                                                                                                                   Katches
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                           / Match 6.4%; Score 104.5; DB 12; Length 1130;
Local Similarity 16.9%; Pred. No. 0.86;
nes 70; Conservative 64; Mismatches 124; Indels 155; Gaps 13;
664 NNLTDQVRNIAEVTTAVAKGDLSRKITVDAKGEVLELKSTINTMVDQLNSFAAEVTRVAK 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356 LYRSP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 IAKLITYGNSREEAIARMKRALREYVIIGVKTNIPFH 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 IDOLKAWGG--ETTSVRENSGIEEKVVFSIPKELKKH 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 VVGSPNSSNSNRLREIAVQLGKPAYLIDTYQDLKQDWLEGIEVVGVTAGASAPEVLVQEV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 -- VTEQVTGIDLVKAMIKIAAGEELTLKQEDVKIRGHAIECRINAEDPLNDFVPCPGKIK 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 AYVTQTTLSMTDTKVMVDALREQFPSIKEQKKDDICYATQ---NRQDAVHDLAKISDLIL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 MQVAKHAKQGREVILIGHAGHPEVEGTMGQYEKCTEGGGIYLVETPEDVRNIKVNNPNDL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 GDPTVFIEKYLENPRHIEIQLLGDKHGNIHLGDRECSIQRRHQKL-IEEAPSPIMTE-- 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 EVVHNRTVVDGLKQKGAVFIEELSDV------PVGSYLI-------FSA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 QKGAVFIBELSDVP--VGSYLIFSAHG----VSKEVQQBAEERQLTVFDATCPLVTKVH 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 GVDRAIBIVDQAI---EAFGAPIYVR-------HEVVHN-RTVVDGLK 50
                                                                                                                                       HGVSKEVQQEAE-----
                                                                                                                                                                                        EVAELADTINAMTQTLSIFAQQVTBVARTVGVEGKLGAQAVVPGVAGTWKDLTNNVNLLA 663
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                                                                                                                                       ---ERQLTV-----
                                                                                                                                     ----FDATCPLVTKVHM 104
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955 AVANGULSQKLTVSVKGEVLELKNTINTMVDQLRAFASEVTRVAKEVGTEGKL 1007		276304 ZONE ZONE ZONE ZONE ZONE ZONE ZONE ZONE	895 LRAFAAEVTRVAKEVGTEGKLGGQADVKDLSGVWKDLTDNVNVLAGNLTDQVRNIAKVTT 954	- !	835 TWKDLTNINVILLANNLTAQVRNIAEVTTAVANGDLSKKITVDAKGEVLELKSTINTMVDQ 894	DL	775 GDLNQKLTMDAKGEIAALADTINAMTQTLSIFAQQVTDVARTVGVEGKLGAQAEVPGVAG 834	154EQFPSIKE 192	724 EVGTEGKLGGQAEVRGVSGVWKDLTDNVNFMAVNLTTQVRGIVRVVTAVAN 774

Search completed: January 29, 2004, 16:21:19 Job time : 22.7073 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: January 29, 2004, 15:44:49; Search time 9.35661 Seconds (without alignments)

108-09-941-947A-18

Perfect score: 1623
Sequence: 1623
Sequence: 1623
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
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F81362	G70449	AC1256	m	6995	w	D37152	72	F86617	G72006	B71461	E87151	D70898	E70973	AE3434	F97453	AH2671	G87665	A84947	C82561	103	416	229	G85483	H90632	JE0403	AD0508	AC0059	G83076	1	
B homolog C	ytB protein	Ĕ. coli LytB prote	penicillin toleran	ř	3	lytB protein homol	penicillin toleran	metalloproteinase	pemicillin toleran	probable metallopr	LytB homolog [impo	probable lyth' pro	probable lytB prot	lytB protein [impo	protein	cillin to	protein	protein [tolerand	protein	protein	protein	thetical	B protein (i	B protein	protein	B protein [imp	LytB protein PA455	criptio	

RESULT 2

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	108.5	109	109	109	109	110	111.5	112.5	115	230	288	312	332	335.5	341	358
	6.7	6.7	6.7	6.7	6.7	6. B	6.9	6.9	7.1	14.2	17.7	19.2	20.5	20.7	21.0	22.1
	544	925	578	522	499	500	777	434	929	452	376	402	275	274	406	642
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	B41479	G88175	B70796	A33644	AI1472	AB1111	G69773	B72228	T35683	T04781	G71310	AF1929	A72253	H64569	S76307	H97127
•	60K heat shock pro	protein T24H7.2 [i	probable DNA POLYM	signal recognition	heat-shock protein	heat-shock protein	conserved hypothet	pyrimidine-nucleos	ftsk homolog - Str	hypothetical prote	probable penicilli	hypothetical prote	lytB protein - The	lysis tolerance pr	hypothetical prote	fusion Penicillin

ALIGNMENTS

Qy 301 EEKVVFSIPKBLK 313 Db 298 EENITFSMPKELR 310	QY 241 GKPAYLIDTYQDLKQDWLEGIEVVGVTAGASAPEVLVQEVIDQLKAWGGETTSVRENSGI	OY 181 DALREQFPSIKEOKKODICYATQNRODAVHDLAKISDLILYVGSPNSSNSNELREIAVOL 	Qy 121 HAGHPEVEGTMGQYEKCTEGGGIYLVETPEDVRNILKVNNPNDLAYVTQTTLSMTDTKVMV	Qy 61 SDVPVGSYLIFSAHGVSKEVQQEABERQLTVFDATCFLVTKVHMQVAKHAKQGREVILIG	Qy 1 MQIVLANPRGFCAGVDRAIBIVDQAIBAFGAPIYVRHBVVHNRTVVDGLKQKGAVFIEEL	Query Match 63.4%; Score 1028.5; DB Best Local Similarity 63.3%; Pred. No. 6.8e-67; Matches 198; Conservative 49; Mismatches 63	O> B:AE004869; GB:AE004091; : strain PAO1 llin tolerance protein	.; Olson, M.V. 959-964, 2000 omplete genome sequence e number: A82950; MUID: n: G83076	RESULT 1 G83076 G83076 LytB protein PA4557 [imported] - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text C;Accession: G33076 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger,
	VLVQEVIDQLKAWGGETTSVRENSGI 300 : : ; ; VLVRGVIAQLREWGASEEQELEGR 297	CISDLILVVGSPNSSNSNRLREIAVOL 240 :: QCDMVLVVGSPNSSNSNRLREIAERM 239	NLKVNNPNDLAYVTQTTLSMTDTKVMV 180	ATCPLVTKVHMQVAKHAKQGREVILIG 120 	YVRHEVVHNRTVVDGLKQKGAVFIEEL 60	DB 2; Length 314; e-67; 63; Indels 3; Gaps 2;	NID:g9950793; PIDN:AAG07945.1; GSPDB:GN00	osa PA01, an opportunistic	ruginosa (strain PAO1) 000 #text_change 31-Dec-2000 chi, S.D.; Warrener, P.; Hickey, M.J.; B ; Folger, K.R.; Kas. A.; Larbig, K.; Lim

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Lyth protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18 C;Species; Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AD0508
                                                                                                                                                                                                                                      , S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AD0508
                                                                                                                                                                                                                                                                                                                                                                       R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarrage, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AC0059
                                                    A;Gene: STY0058
C;Superfamily:
                                                                                                                          A;Status; preliminary
A;Molecule type: DNA
A;Residues : 1-316 <2PAR>
A;Cross-references: GB:AL513382; PIDN:CAD01204.1; PID:g16501333; GSPDB:GN00176
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AC0059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8050GA
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A; Residues: 1-317 < KUR>
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  Query Match
                                                                                                               ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 200;
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Best Local
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                                                                                    STYOOSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GHAGHPEVEGTMGQYEKCTEGGGIYLVETPEDVRNEKVNNPNDLAYVTQTTLSMTDTKVM 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEVPDGSILIFSAHGVSQAVRABARSRNLTMLFDATCPLVTKVHMEVARASRKGKEAILI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MQILLANDRGFCAGVDRAISIVERAIEMYGAPIYVRHEVVHNRYVVESLCERGAIFIEEI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGKPAYLIDSAADIQEFWLQGAKCIGVTAGASAPDILVQQVIARLKDLGAGESI---ELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDALREQFESIKEQKKODICYATQNRQDAVHDLAKISDLILVVGSPNSSNSNRLREIAVQ 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHAGHPEVRGTMGQYS--NPNGGMYLVESPDDVWQLNVKDENNLCFMTQTTLSVDDTSAV 178
                                                    penicillin tolerance protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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  61.7%; Score 1001;
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  DB 2;
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A;Residues: 1-316 <BLAT>
A;Residues: 1-316 <BLAT>
A;Cross-references: GB:AE000113; GB:U00096; NID:g2367095; PIDN:AAC73140.1; PID:g178621
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:D10483; NID:g216434; PIDN:BAA01307.1; PID:g216456
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1433-1462, 1997
B;Title: The complete genome sequence of Escherichia coli K-12.
                                                                                                                                                                                                                           A;Gene: lyts
C;Superfamily: penicillin tolerance protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ryvera, T., Mori, H., Nagai, H., Nagata, T., Ishihama, A., Fujita, N., Isono, K., Mizol submitted to the EMBL Data Library, December 1992 A;Description: Systematic sequencing of the Escherichia coli genome: analysis of the O. A;Reference number: S40531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A64720; MUID: 97426617; PMID: 9278503
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A; Residues: 1-316 < YUR>
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A; Residues: 1-316 < BOU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Bouvier, J.; Stragier, P.
Nucleic Acids Res. 19, 180, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lytB protein - Escherichia coli (strain K-12)
C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: nucleic acid sequence not shown; translation not shown
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C;Accession: JE0403; S40552; E64723; S22290
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61 SDVPVGSYLIFSAHGVSKEVQQBAEERQLTVFDATCFLVTKVHMQVAKHARQGREVILIG 120
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                                                                                                                                                  61.4%; Score 996; DB 2; 61.3%; Pred. No. 1.5e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H.; Nagata, T.; Ishihama, A.; Fujita, N.; Isono, K.; Mizolibrary, December 1992
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C; Superfamily:
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genca; Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H90632
RESULT
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
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A; Residues: 1-316 <HAY>
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Matches 192;
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;Species: Escherichia coli
;Date: 10-Jul-2001 #sequence_revision 10-Jul-2001 #text_change 03-Aug-2001
;Accession: H90632
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                                                                                                                       GKRAFLIDDAKDIQEEWVKEVKCVGVTAGASAPDILVQNVVARLQQLGGGEAIPLE--GR
                                                                                                                                         GKPAYLIDTYQDLKQDWLEGIEVVGVTAGASAPEVLVQEVIDQLKAWGGETTSVRENSGI 300
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Pred. No. 1.5e-64;
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-320 <HEI>
A;Cross-references: GB:AE004154; GB:AE003852; NID:g9655115;
A;Experimental source: serogroup OI; strain N16961; biotype
                                                                                                                                                                                                                                                                                                                             R;Heidelberg, J.F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwir chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; l, R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: G82293
A; Map position:
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lytB protein VC0685 [imported] - Vibrio cholerae (strain N16961 serogroup O1) (Species: Vibrio cholerae C. Decies: Vibrio cholerae C. Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C. Accession: G82293
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                                                                               A;Gene: VC0685
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A;Residues: 1-316 <STO>
A;Croos-references: GB:AE005174; NID:g12512712; PIDN:AAG54331.1; GSPDB:GN00145; UWGP:Z00: A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: lytB
C;Superfamily: penicillin tolerance protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       片
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                                                                                                                   Genetics:
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                                       position: 1
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   penicillin tolerance protein
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; Pred. No. 1.5e-64;
59; Mismatches 58
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H.; Dragoi, 1
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                                                                                                                                                                                          GSPDB:GN001;
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Query

Score 987;

DB 2;

Length 320;

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A; Residues: 1-318 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Authors: Gnehm, C.I.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
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C;Species: Haemophilus influenzae
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                                                                                                                            181
                                                                                                                                                                                             121 HAGHPEVEGTMGQYEKCTEGGGIYLVETPEDVRNLKVNNPNDLAYVTQTTLSMTDTKVMV
                                                                                                                                                                                                                                                                                                                                                                        184;
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                                                                                         AALKEKYPAIQGPHKNDICYATTNRQEAVRELAKLSDLVLVVGSKNSSNSNRLAELASRM
                                                                                                                      DALREQFPSIKEQKKDDICYATQNRQDAVHDLAKISDLILVVGSPNSSNSNRLREIAVQL
                                                                                                                                                                                                                                                   SDYPYGSYLIFSAHGYSKEYQQEAEERQLTYFDATCPLYTKYHMQYAKHAKQGREYILIG
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                        GVKSQLLDEPADIQADWFNDVKTIGITAGASAPEELGQSIISRLKRFG--ANSIEELQGL
                                                    GKPAYLIDTYQDLKQDWLEGIEVVGVTAGASAPEVLVQEVIDQLKAWGGETTSVRENSGI
                                                                                                                                                                                                                                                                                                                          MQIVLANPRGFCAGVDRAIEIVDQAIEAFGAPIYVRHEVVHNRTVVDGLKQKGAVFIEEL
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                                                                                                                                                            HKGHPEVEGTMGQYS--NEDGGIFLIEKVEDIARLPMQENDNLTFMTQTTLSLDDTAETI
                                                                                                                                                                                                                               SEVPDGAIVIFSAHGVSQAVRQEAKDRNLKVFDATCPLVTKVHMQVARASRKGTKAILIG
                                                                                                                                                                                                                                                                                                   MKIILANPRGFCAGVDRAISIVELALEIHGAPIYVRHEVVHNRFVVNGLRERGAIFVEEL
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                                                                                                                                                                                                                                                                                                                                                                                         58.88;
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                                                                                                                                                                                                                                                                                                                                                                                       Score 969; DB 1;
Pred. No. 1.4e-62;
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6; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                        Length 31B;
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                    RBSULT 10
C82561
drug tolerance protein XF2416 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
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C; Superfamily:
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A; Residues: 1-322 < TET >
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
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Best Local S
Matches 192
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Pred. No. 1.7e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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A;Cross-references: GB:AB002532; GB:AB002098; NID:g7227078; PIDN:AAF42166.1; PID:g722708
A;Experimental source: serogroup B, strain MC58
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: D81982
A;Scatus: preliminary
A;Molecule type: DNA
A,Roseidance 1799: DNA
A,Roseidance 1799: DNA
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A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R. A;Tille: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A;Reference number: A81000; MUID:20175755; PMID:10710307
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A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83914.1; PID:g737935
A;Experimental source: serogroup A, strain Z2491
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                                                                                                                                                                                                                                                                                                                                                                                                                  183 LREQFPSIKEQKKDDICYATQNRQDAVHDLAKISDLILVVGSPNSSNSNRLREIAVQLGK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 VPPGATLVYSAHGVSKAVRQEAAERGFRVFDATCPLVTKVHKEVARLDAQDCEIIMIGHK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 IVLANPRGFCAGVDRAIBIVDQAIBAFGAPIYVRHEVVHNRTVVDGLKQKGAVFIBBLSD 62
DAYMYDNAGYLQRAMFEGKNKYGYTAGASAPEYLYREYLATIRGWGHET--VREGEGAEE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GHPEVEGTMGQYEKCTEGGGIYLVETPEDVRNLKVANMPNDLAYVTQTTLSWTDTKVMVDA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPVGSYLIFSAHGVSKEVQQEAEERQLTVFDATCPLVTKVHMQVAKHAKQGREVILIGHA 122
                                                                                                                                        PAYLIDTYQDLKQDWLBGIEVVGVTAGASAPEVLVQEVIDQLKAWGGETTSVRENSGIEE 302
                                                                                                                                                                                                                                                                                 LNARFPNIRNPHKEDICYATTNRQTAVKELAEQCDIVIVVGSPNSSNSNRLREVAASRGI
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C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02:
C;Accession: A84947
R;Shigenobu, S.; Watanabe, H.; Hattori, M
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellu:
A;Reference number: A84930; MUID:20445173
A;Accession: A84947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Abriones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, A.A.; Carraro, D.M.; Carrer, Has-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laiguchado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.R.; Rodrigues, V.; Rosa, A.U. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, A;Reference number: A59328
A;Contents: annotation
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C;Superfamily:
A;Status: preliminary A;Molecule type: DNA
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A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 c;Accession: C82561
R;Annonymous, The Xylella fastidiosa Consortium of the Organization for Nucle Nature 406, 151-157, 2000
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A; Residues: 1-316 < SIM>
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                                                                 sequence of the endocellular bacterial symbiont ber: A84930; MUID:20445173; PMID:10993077
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61.0%;
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; Pred. No. 1.9e-62;
wismatches 67;
                                                                                                                                                                                                                           sp.
                                                                                                                                                                          02-Mar-2001 #text_change 23-Mar-2001
                                                                                                                                                                                                                              (strain APS)
                                                                                                                              M.; Sakaki, Y.; Ishikawa,
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; pMID:11259647
A;Accession: G87665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-319 <STO>
A;Cross-references: GB:AP000398;
A;Experimental source: strain APS
C;Genetics:
A;Gene: lytB; BU147
C;Superfamily: penicillin toleran
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE005673; NID:gl3425065; PIDN:AAK25323.1; GSPDB:GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IytB protein [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Apace : 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: G87665
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Best Local S
Matches 172
                                                                                                                                                                                                                                                                                                                                                                                     ;Superfamily: penicillin tolerance protein
                                                                                                                                                                                                                                                                                                                                                                                                                ;Gene: CC3361
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                                                                                                                                                                                                                                     MQIVLANPRGFCAGVDRAIEIVDQAIEAFGAPIYVRHEVVHNRTVVDGLKQKGAVFIEEL
                   HAGHPEVIGTMGQLPE----GAVTLIEDLKDAAAWEPKDAANVAFLIQTTLSVDDTADMV
                                                               HAGHPEVEGTMGQYEKCTEGGGIYLVETPEDVRNLKVNNPNDLAYVTQTTLSMTDTKVMV
                                                                                                             EEAPDDRPVVFSAHGVPKSVPAEAKARQMIYLDATCPLVSKVHVEAQKHYDAGREIVLIG
                                                                                                                                      SDYPYGSYLIFSAHGYSKEYQQEAEERQLTVFDATCPLVTKYHYQYAKHAKQGREVILIG
                                                                                                                                                                                                     | SIVLASPRGECAGUDRAIQIVERAVEKFGAPVYVRHEIVHNRHVVDRLKALGAVFIEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQIPDYSVVIFSAHGVSKKVVQBAVKKLIILDATCPLVBKVHIEVSKSSEKAIETILIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REKVVFSIPKEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AALKNKFPEISGPNKEDICYATTNRQIAVRQLSKIADIIFVIGSNNSSNSNRLAELGKET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HRGHPEVEGTIGQYN--NKNGKIYLVESIEDVHNLSVQNSKKLNFFTQTTLSITNTKKII 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDVPVGSYLIFSAHGVSKEVQQEAEERQLTVFDATCPLVTKVHMQVAKHAKQGREVILIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MQIVLANPRGFCAGVDRAIBIVDQAIBAFGAPIYVRHEVVHNRTVVDGLKQKGAVFIBEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTFTKLISSFLDIKKKWLKNVNYIGITAGASAPBILVTEVIQYLRKIGAHKPI--EMIGV
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                                                                                                                                                                                                                                                                                             ; Score 826.5; DB 2;
; Pred. No. 2.7e-52;
48; Mismatches 86;
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Pred. No. 1.4e-54;
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                                                                                                                                                                                                                                                                                               Indels
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7;

Gaps

70 60

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lytB protein (AE006203) [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C;Accession: F97453
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                                                                                             RESULT 14
F97453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: AH2671
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; erage, G.; Gillet, W.; Grant, C.; Guenthmer, D.; Kutyavin, T.; Levy, R.; Li, M.; W.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: circular of C; Superfamily: penicillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA_A; Molecule type: DNA_A; Restitues: 1-348 <KUP>
A; Restitues: 1-348 <KUP>
A; Cross-references: GB: AE008688; PIDN: AAL41790.1; PID: 917739144; GSPDB: GN00186
A; Experimental source: strain C58 (Dupont)
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A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ster,
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                                                                                                                                                                                                                              RENSGIEEKVVFSIPKELK 313
                                                                                                                                                                                                                                                                        LRAGAKHSVLVQRASEI--DWNEIGDIRTVGLSAGASAPEVIVDEIIEAFKARFDTTLDL
                                                                                                                                                                                                                                                                                                                   VQLG-KPAYLIDTYQDLKQDWLE--GIEVVGVTAGASAPEVLVQBVIDQLKAWGGETTSV 294
                                                                                                                                                                                                                                                                                                                                                             GVIARLQERFPAIQAPAADSICYATTNRQDAVKQAAPGCDLFIVVGAPNSSNSKRLVEVA
                                                                                                                                                                                                                                                                                                                                                                                                       VMVDALREQFPSIKEQKKDDICYATQNRQDAVHDLAKISDLILVVGSPNSSNSNRLREIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIGHAGHPEVIGTMGQLPE----GTVSLVETVEDAGVYEPVDRENLGFVTQTTLSVDDTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIGHAGHPEVBGTMGQYEKCTEGGGIYLVETPEDVRNLKVNNPNDLAYVTQTTLSMTDTK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDVPV---GSYLIFSAHGVSKEVQQEABERQLTVFDATCPLVTKVHMQVAKHAKQGREVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARETITEKLPRLL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-KPAYLIDTYQDLKQDWLEGIEVYGVTAGASAPEVLVQEVIDQLKAWGGETTSVRENSG
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                                                                                                                                                                                    AVT--VEETEHFLVNRELR 320
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Pred. No. 3.7e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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LEIRLCGPRGFCAGVDRAIQIVVLALKKYGAPVYVRHEIVHNRYVVBGLQARGAIFVEEL

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lyte protein [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C;Accession: AE344
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
; Mazur, M.; Goltsman, B.; Selkov, E.; Blzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AB3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldt A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: F97453

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-348 <KUR>
                   Ś
                                                                                                                                                     A;Gene: BMEI1459
A;Map position: I
C;Superfamily: penicillin tolerance protein
                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-346 <KUR>
A;Cross-references: GB:AB008917; I
A;Experimental source: strain 16M
C;Genetics:
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A;Map position: circular chromosome
C;Superfamily: penicillin tolerance protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 HEIPAEHREQPVVFSAHGVPKSVPEDAQARNLFYLDATCPLVSKVHKQAMRHQRLGRHVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 LTIRLCGPRGFCAGVDRAIQIVVLALKAYGAPVYVRHEIVHNRYVVEGLEAKGAIFVEEL
                                                                                         Similarity
MQIVLANPRGFCAGVDRAIEIVDQAIEAFGAFIYVRHEVVHNRTVVDGLKQKGAVFIEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVT -- VEETSHFLVNRELR 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDVPV----GSYLIFSAHGVSKEVQQEAEERQLTVFDATCPLVTKVHMQVAKHAKQGREVI 117
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                                                                     Conservative
                                                                   46.2%; Score 750; DB 2
47.7%; Pred. No. 1e-46;
tive 59; Mismatches
                                                                                                                                                                                                                                                                            PIDN:AAL52640.1; PID:g17983462; GSPDB:GN00190
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kelz, B.;
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Db 68 DEIPAAHRNOPVVPSAHGVPKSVPADAEAK Qy 118 LIGHAGHPEVEGTMGQYEKCTEGGGIYLVE Db 128 LIGHSGHPEVIGTMGQYLPDGAVTILIE Db 128 LIGHSGHPEVIGTMGQLPDGAVTILIE CY 178 VMVDALREQFPSIKEQKUDICYATQMROP 184 GIIKELQARFPNLAAPAAESICYATTMROD CY 238 VQLG-KPAYLIDTYQDLKQDMLEGIEVVGV 184 GIIKELQARFPNLAAPAAESICYATTMROD CY 238 VQLG-KPAYLIDTYQDLKQDMLEGIEVVGV 1	Ş
DEIPAAHRNOPVPSSHGVPKSVPF LIGHAGHPEVEGTMGQYEKCTEGGG	61
NLFYLDATCDLVSKVHKQAMRHQRLGRHVI TPEDVRNLKVNNPNDLAYVTQTTLSMTDTK	61 SDVPVGSYLLFSAHGYSKEVQQEAEERQUTVFDATCPLYTKYHMQVAKHAKQGREVI 117

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Minimum
Maximum
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Maximum Match 100%
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      Score
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1623
1 MQIVLANPRGFCAGYDRAIE......GIEEKYVFSIPKELKKHMQA 318
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Q8det0 vibrio vuln
Q9ku44 vibrio chol
Q8pu17 xanthomonas
Q8pbg4 xanthomonas
P44976 haemophilus
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61 SDVPVGSYLIFSAHGVSKEVQQEAEERQLTVFDATCPLVTKVHMQVAKHAKQGREVILIG

120 60

QVPDDSIVIFSAHGVSKAVQQBABHRGLKVFDATCPLVTKVHIBVTKYARBGTEAILIG

Conservative

65.6%; Score 1064.5; DB 1; Length 65.2%; Pred. No. 2.1e-68; tive 48; Mismatches 58; Indels

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, AADS5804.1; , -, 1 3451; LYtB. LYTB; 1. LYTB; 1. 0216; ispH_lytB theeis. the; 34943 MW;	SS-PROT entry is copy the Swiss Institute the Swiss Institute seam Bioinformatics non-profit institute and this statement requires a license in memail to licensee.	FROM N.A. 9413 / ADP1; 9413 / ADP1; 9424835; PubMed=10763755 C., Friedrich A., Averho novel competence gene re acter sp. BD413: identifi phase-dependent regulat rocbiol. 173:220-228 (2007) FION: Converts 1-hydroxy- isopentenyl diphosphate p) (By similarity). AX: Nonmevalonate terpen step. step. step. step. step. step. step. step. step. step. step.	11. 41, Created 11. 41, Last se 11. 41, Last an 11. 41, Last an malcoaceticus. sobacteria; Gam Acinetobacter.	311 331 331 331 66289 66289 60289 70379 77274 57274 57275	180 335 314
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CRC64;	hrough a colla the EMBL outs restrictions ontent is in by and for cow.isb-sib.ch/a	al transformation of rization and analysis utenyl 4-diphosphate ylallyl diphosphate pathway; seventh	Pseudomonadales;		p21864 pseudomonas Q9rsg0 deinococcus p544473 bacillus su

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16-OCT-2001
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STRAIN-ANTCC 15692 / PAO1;

MEDLINE=20437337; PubMed=10984043;

MEDLINE=20437337; PubMed=10984043;

Scover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Smith K.A., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                              HAMAP; MF 00191; -; 1.
InterPro; IPR003451; LytB.
Pfam; PF02401; LYTB; 1.
FIGR0716; ispH lytB; 1.
Isoprene biosynthesis; Complete proteome.
SEQUENCE 314 AA; 34762 MW; 4B3E07B68663EEE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
Nature 406:959-964(2000).
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ISPH OR LYTB OR PA4557
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SIMILARITY: BELONGS TO THE ISPH FAMILY.
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Score 1028.5;
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19; Mismatches
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This SWISS-PROT entry is copyright. It is produced through a collab-
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modified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                                                                                                  "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
-!- FUNCTION: Converts 1-hydroxy-2-methyl-2-(E)-butenyl.
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Derg W., Burland V., Punnkett G. II, Boutin A., Mayb
Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.
Petherston J.D., Lindler L.B., Brubaker R.R., Plano G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebakhia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Peltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome seguence of Yersinia pestis, the causative agent of plague."
Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=KIM5 / Biovar Mediaevalis;
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STRAIN=CO-92 / Biovar Orientalis;
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ISPH OR LYTB OR YPO0477 OR Y3697
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SIMILARITY: BELONGS TO THE ISPH PAMILY.
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(Rel. 41, Last sequence up
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                                                                                                                                                                                                                                           terpenoid biosynthesis pathway;
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P58678;
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                                                                       MEDILINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Peltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi (T18.";
Nature 413:848-852(2001).
SEQUENCE FROM N.A.
STRAIN=Ty2 / ATCC 700931;
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=CT18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella typhi.
Bacteria; Proteobacteria; Gammaproteobacteria;
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HAMAP; MF 00191; -; 1.
InterPro; IPR003451; LytB.
Pfam; PF02401; LYTB; 1.
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EMBL; AE013973; AAM87245.1;
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TIGREAMS; TIGRO0216; ispH_lytB; 1.
Isoprene biosynthesis; Complete proteome.
SEQUENCE 317 AA; 34708 MW; C40E953DCBA12168 CRC64;
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Best Local Sim
Matches 195;
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5.L1
Escherichia coli,
Escherichia coli 06, and
Escherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaj
Enterobacteriaceae; Escherichia.
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01-AUG-1991 {Rel. 19, Last seq
28-FEB-2003 {Rel. 41, Last ann
                                                                         ISPH OR LYTB OR B0029
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EMBL; AE016834; AA067784.1;
HAMAP; MF_00191; -; 1.
InterPro; IPR003451; LytB.
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-I: FUNCTION: Converts 1-hydroxy-2-methyl-2-(B)-butenyl 4-diphosphate into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP) (By similarity).

-I: PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; seventh
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Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.,
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
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AMs; TIGRO0216; ispH_lytB; 1.
ene biosynthesis; Complete proteome.
NCE 316 AA; 34513 MW; 9536031F11F6DC42 CRC64;
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              Gammaproteobacteria; Enterobacteriales;
                                                                                                         annotation update)
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                                                                                                                         sequence update)
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Pred. No. 6.7e-64;
3; Mismatches 61;
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STRAIN-0157:H7 / EDI933 / ATCC 700927;

STRAIN-0157:H7 / EDI933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

Merland V., Mau B., Glasner J.D.,

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., 3vans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., 3vans P.S., Gregor J., Kirkpatrick H.A.,

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Posfai G., Hackett J., Klink S., Dimalanta E.T., Potanousis K.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potanousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                               STRAIN=0157:H7 / RIMD 0509952;

MEDLLNB=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii Hana C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N Kuhara S., Shiba T., Hattori M., Shinagawa H., Schari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bouvier J., Stragier P.;
"Nucleotide sequence of the lsp-dapB interval in Escherichia coli.";
Nucleic Acids Res. 19:180-180(1991).
MEDLINE=93163053; PubMed=8432714;
Gustafson C.E., Kaul S., Ishiguro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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                                                                   "Complete genome sequence of enterohemorrhagic Escherichia O157:H7 and genomic comparison with a laboratory strain K-1DNA Res. 8:11-22{2001}.
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=06:H1 / CFT073 / ATCC 700928;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Systematic sequencing of the Escherichia the 0-2.4 min region.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21819424; PubMed=11818558;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Studies on the nonmevalonate terpene biosynthetic pathway: metabolic
                                  IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=562,
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                                                                                                                                                                                                                                                                                           ca J., Anantharaman
R.A., Blattner F.R.
                                                                                                                                                                                                                                                            409:529-533 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .4 min region.";
Acids Res. 20:3305-3308(1992).
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hi K., Nakata A.;
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"The lytB gene of Escherichia coli is essential and specifies a product needed for isoprenoid biosynthesis.";

J. Bacteriol. 183:7403-7407(2001).

-i- FUNCTION: Converts 1-hydroxy-2-methyl-2-(3)-butenyl 4-diphosphate into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (IMAPP). Is also involved in penicillin tolerance and control of the stringent response. Seems to directly or indirectly interact with relA to maintain it in an inactive form during normal growth.
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PIR; H90632; H90632.
PIR; JE0403; JE0403.
EcoGene; EG11081; ispH.
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InterPro; IPR003451; LytB.
Pfam; PF02401; LYTB; 1.
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SIMILARITY: BELONGS TO THE ISPH FAMILY.
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D10483; BAB96598.1; -.
D104031; AAC73140.1; -.
AE016755; AAX78533.1; ALT_INIT.
AE005179; AAG54331.1; -.
AP002550; BAB33455.1; -.
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biosynthesis; Complete
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                                               DALREOFPSIKEOKKODICYATONRODAVHDLAKISDLILVVGSPNSSNSNRLREIAVQL
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STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDIINE=21534948; PubMed=11677609;
MCClelland K., Sanderson K.E., Spieth J., Clifton S.W., Latreille P. Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                     HAMAP; MF_00191; -; Î.
InterPro; TPR003451; LytB.
Pfam; PF02401; LYTB; 1.
TIGREAMS; TIGR00216; ispH_lytB;
Isoprene biosynthesis; Complete
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28-FEB-2003
28-FEB-2003
28-FEB-2003
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ISPH OR LYTB OR STM0049.
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Best Local :
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EMBL; AP005074; BAC58800.1; -.
HAMAP; MF 00191; -; 1.
Isoprene biosynthesis; Complete proteome.
SEQUENCE 321 AA; 35721 MN; DFEB4ABA39970798 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the ENropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K. Tijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S. Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T., "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae.";
Lancet 361.743-749(2003).
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Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- FUNCTION: Converts 1-hydroxy-2-methyl-2-(S)-butenyl 4-diphosphate (IPP) and dimethylallyl diphosphate (IMAPP) (By similarity).
-i- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; seventh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE ISPH FAMILY.
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MEDLINE=22508454; PubMed=12620739;
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ISPH OR LYTB OR VP0537.
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15-SEP-2003 (Rel.
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                                                   121 HAGHPEVEGINGQYEKCTEGGGIYLVETPEDVRNIK--VNNPNDLAYVTQTELSMTDTKV 178
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HAGHPEVBGTMGQYS--SETGGMYLVETPADVEKLKAIVKDPSDLHYVSQTTLSVDETAD
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61.9%; Pred. No. 4.5e-63;
tive 54; Mismatches 61
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Pf4m; PF02401; LYTB; 1.
TIGRPAMs; TIGR00216; ispH_lytB; 1.
Isoprene biosynthesis; Complete proteome.
SEQUENCE 320 AA; 35575 MH; 09FB454ACDA1EIDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a content to the swiss Institute of Bioinformatics and the SWBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE016798; AA009023.1; -. HAMAP; MF_00191; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of Vibrio vulnificus CMCP6."; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IspH protein.
ISPH OR LYTB OR VV10504.
Vibrio vulnificus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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-!- SIMILARITY: BELONGS TO THE ISPH FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway;
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15-SEP-2003
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(DMAPP) (By similarity)
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HAGHPEVEGTMGQYASLQ--GGMYLVEKPEDVLGLKAIVKDPSNLHYVSQTTLSVDETAD
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(Rel. 42, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chung S.S., Kim J.J., Moon Y.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                 Score 989; DB
Pred. No. 4.8e
52; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                 4.8e-63;
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                                                                                                     Query Match
Best Local
                                                                                Matches
                                                                                                                                                                                                                                                              EMBL; AB004154; AAF93850.1; ALT_INIT.
TIGR; VC0685; -.
HAMAP; MF 00191; -; 1.
InterPro; IPR003451; LytB.
Pffam; PF02401; LYTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 406:477-483(2000).
Nature 406:477-483(2000).
-!- FUNCTION: Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
-into isomentenyl diphosphate (IPP) and dimethylallyl diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O. Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C Fraser C.M.;
                                                                                                                                                                                   TIGRFAMs; TIGR00216; ispH lytB; 1.
Isoprene biosynthesis; Complete pr
SEQUENCE 316 AA; 35156 MW; BB3
                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=El Tor N16961 / Serotype O1;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Bisen J.A., Nelson W.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vibrio cholerae.
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28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
Vibrionaceae; Vibrio,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
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ISPH OR LYTB OR VC0685.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (last) step.
SIMILARITY: BELONGS TO THE ISPH FAMILY.
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                                                                                195;
                                                                                                           Similarity
MQIVLANPRGFCAGVDRAIBIVDQAIBAFGAPIYVRHEVVHNRTVVDGLKQKGAVFIEEL
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                                                                              Conservative
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                                                                              56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence update)
                                                                           Score 987; DB 1;
Pred. No. 6.6e-63;
66; Mismatches 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clayton R.A.,
                                                                                58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Usage
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                                                                                                                                  Length 316;
                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pathway; seventh
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Venter J.C.,
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RX MEDLINE=2022145; PubMed=12024217;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

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RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Cicarelli R.M.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

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RA Formighieri E.F., Machado M.A., Madeira R.M.B.N., Martinez-Rossi N.M.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Martins B.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Moreira H.A., Rossi A., Sen J.A.D., Silva C., de Souza R.F.,

RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

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RA Spinola L.A.F., Takita M.A., Truffi D., Tsai S.M., White F.F.,

RA Setubal J.C., Kitajima J.P.;

RT Montarison of the genomes of two Xanthomonas pathogens with differing

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  EMBL; AE011755; AAM36128.1;
HAMAP; MF_00191; -; 1.
InterPro; IPR003451; LytB.
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISPH protein.
ISPH OR LYTB OR XAC1256
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                                                                                                                                                                                                                                                                                                   (last) step.
SIMILARITY: BELONGS TO THE ISPH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Converts 1-hydroxy-2-methyl-2-(E)-butenyl into isopentenyl diphosphate (IPP) and dimethylallyl (DMAPP) (By similarity).
                                                                                                                                                                                                                                                                                                                                                   PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; seventh
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation updat
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Best Local S
Matches 192
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Q8PBG4;
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Bacteria; Proteobacteria;
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28-FEB-2003 (Rel.
28-FEB-2003 (Rel.
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. 41, Last sequence.
. 41, Last annotation.
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RC STRAIN-ATCC 3913 / NCPPB 528;
RC MEDLINE-ATCC 3913 / NCPPB 528;
RR MEDLINE-20022145; PubMed-1202427;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
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RA Actauyama A.M., Kishi L.T., Leate R.P., Lemos B.G.M., Lemos M.V.F.,
RA Actauyama A.M., Kishi L.T., Leate R.P., Lemos B.G.M., Lemos M.V.F.,
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RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Moreira L.M., Rossi A., Sena J.A.D., Silva C., de Souza R.P.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.P.,
RA Pinnola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
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RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
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RA Trindade dos Santos M., Tsai S.M., White F.F.,
RA Trindade dos Santos M., Tsa
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TIGREAMS; TIGRO0216; isph_lytB; 1.
Tigreams; Tigrentesis; Complete proteome.
SEQUENCE 316 AA; 34690 MW; C931226D6A53D4DA CRC64;
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STRAIN=Rd / KW20 / ATCC 51907;

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MEDLINE=95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Rerlavage A.R., Bult C.J., Tomb J.F., Dougherty B.A., Merrick J.M., Kerlavage R.R., Bult C.J., Tomb W.F., Fields C.A., Gocayne J.D., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Kelley J.M., McKenney K., Sutton G., Jriu L.-I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Fine C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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STRAIN-Pm70

EQUENCE FROM N.A.

NCBI_TaxID=747; Pasteurellaceae;

Pasteurella.

Gammaproteobacteria;

Pasteurellales;

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RESULT 13
ISPH PASM
ID 16PH
AC P5796
DT 16-OC
DT 16-OC
DT 18PH
GN 18PH
GN 18PH
OS Paste
OC Paste
OC Paste
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ISPH OR LYTB OR PM1664.
Pasteurella multocida.
Bacteria; Proteobacteria;
                                                                                                                                                                                                       PASMU
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGRPAMs; TIGR00216; ispH_lytB; 1.
Isoprene biosynthesis; Complete proteome.
SEQUENCE 314 AA; 34468 MW; 44860D110E9F9EBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions with the property of the institutions as long as its content is in modified and this statement is not removed. Usage by and for contentities requires a license agreement (See http://www.isb-sib.ch/aror send an email to license@isb-sib.ch).
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PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; seventh
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                                                                                                                                                                                                                                                                                                                        GVKSQLLDEPADIQADWFNDVKTIGITAGASAPBELGQSIISRLKRFG--ANSIEELQGL
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(Rel. 41,
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                                                                                                                                                                                        STANDARD;
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28-FEB-2003 (Rel. 41, Created)
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28-FEB-2003 (Rel. 41, Last annotati
1spH protein.
ISPH OR LYTE OR NMA0624 OR NMB1831.
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as lits content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                             Neisseria meningitidis (serogroup A), and
Neisseria meningitidis (serogroup B).
Neisseria, Proteobacteria; Betaproteobacte
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Pfam; PF02401; LYTB; 1.

TIGREAMS; TIGR00216; ispH_lytB; 1.

Isoprene biosynthesis; Complete proteome.

SEQUENCE 314 AA; 34469 MW; DCB6179787883125 CRC64;
 SEQUENCE FROM N.A.
STRAIN=Z2491 / Sel
                                   NCBI_TaxID=65699, 491;
                                                     Neisseriaceae; Neisseria.
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PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; seventh
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                                                                                                                                 (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation updat
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Serogroup
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                                                                  Betaproteobacteria;
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Pred. No. 1.2e-61;
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Best Local :
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InterPro; IPR003451; LytB.
Pfam; PF02401; LYTB; 1.
TIGRRAMs; TIGR00216; ispH_lytB; 1.
Isoprene biosynthesis; Complete proteome.
SEQUENCE 322 AA; 35322 MW; 6E92762C06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL162753; CAB83914.1;
EMBL; AE002532; AAF42166.1;
PIR; D81038; D81038.
TIGR; NMB1831; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-MCS8 / Serogroup B;

MEDLINE-2017575; PubMed=10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,

Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,

Nelson T., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,

Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,

Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,

Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;

"Complete genome sequence of Neisseria meningitidis serogroup B strain

"Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=2022556; PubMed=10761919;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491.";
"Strain Scales Controls"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i. FUNCTION: Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMA,PP) (By similarity).
-i. CAMERAY: Nonmevalonate terpenoid biosynthesis pathway; seventh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 287:1809-1815(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - i - SIMILARITY: BELONGS TO THE ISPH FAMILY.
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                     243
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                                                                                                                                                                                                                                                                                                                                                                               192;
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                                                                                                                                                                                                                                                                                                                      IVLANPRGFCAGVDRAIEIVDQAIEAFGAPIYVRHEVVHNRTVVDGLKQKGAVFIEELSD
PAYLIDTYQDLKQDWLEGIEVVGVTAGASAPEVLVQEVIDQLKAWGGETTSVRENSGIEE
                                                                                                                                                                                                                                            VPVGSYLIESAHGVSKEVQQEAEERQLTVFDATCPLVTXVHMQVAKHAKQGREVILIGHA 122
                                                                                                                                                                                                                                                                                                   LREQPPSIKEQKKDDICYATQNRQDAVHDLAKISDLILVVGSPNSSNSNRLREIAVQLGK
                                                                                                                                                                GHPEVBGTMGQYEKCTEGGGIYLVETPEDVRNI.KVNNPNDLAYVTQTTLSMTDTKVMVDA
                                                                                                                                                                                                                     VPPGATLVYSAHGVSKAVRQBAABRGFRVFDATCPLVTKVHKEVARLDAQDCBIIMIGHK
                                                        LNARFPNIRNPHKEDICYATTNRQTAVKELAEQCDIVIVVGSPNSSNSNRLREVAASRGI
                                                                                                                                         GHVEVEGTNGQLAP----GKMLLVETVGDVAKLEVRNPDKLAYVSQTTLSVDETKDIIAA
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                                                                                                                                                                                                                                                                                                                                                                               Score 968; DB 1;
Pred. No. 1.5e-61;
8; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                               6E92762C0653D78F CRC64;
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RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Temecula1 / ATCC 700964;

RC STRAIN=Temecula1 / ATCC 700964;

RX MEDLINE=22421331; PubMed=12333478;

RX MISSINE=22421331; PubMed=12333478;

RA MISSINE=22421331; PubMed=12333478;

RA Missine=22421331; PubMed=12333478;

RA Missine=22421331; PubMed=1233478;

RA Goldman M.H.S. Goldman G.H., Camargo L.E., Goldman G.H., Camargo M.V.F., El-Dorry H., Tsai S.M.,

RA Goldman M.H.S. Goldman G.H., Lemos M.V.F., Il-Dorry H., Tsai S.M.,

RA Goldman M.H.S. Goldman G.H., Lemos M.V.F., Siqueira W.J.,

RA Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Kuramae B.E.,

RA Coutinho L.L., Kimura S.T., Ferro E.S., Harakava R., Kuramae B.E.,

RA Marino C.L., Giglioti E., Abreu I.L., Alves L.M., do Amaral A.M.,

RA Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,

RA Gunha A.F., Fenille R.C., Ferro J.A., Formighteri E.F., Kishi I.T.,

RA Leoni S.G., Oliveira A.R., Rosa V.B. Jr., Sassaki F.T., Sena J.A.D.,

RA Leoni S.G., Oliveira A.R., Rosa V.B. Jr., Sassaki F.T., Sena J.A.D.,

RA Goldman M.H.S., Satubal J.C.,

Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
δ
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ISPH OF MATTE OR XP2416 OR PD1435.
ISPH OF THE OR XP2416 OR PD1435.
Xylella fastidiosa, and
Xylella fastidiosa (strain Temeculal / ATCC 700964).
Xylella fastidiosa (strain Temeculal / ATCC 700964).
Bacteria, Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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     fastidiosa.";
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NCBI_TaxID=2371, 183190;
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42, Last annotation updat
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Matches 191
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SEQUENCE
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-!- FUNCTION: Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
-!- and dimethylallyl diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb
                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP, MF 00191; -; 1.
InterPro; IPR003451; LytB.
Pfam; PF02401; LYTB; 1.
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EMBL; AE012558; AAO29279.1; -.
PIR; C82561; C82561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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SIMILARITY: BELONGS TO THE ISPH FAMILY.
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PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; seventh
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biosynthesis; Complete
316 AA; 34704 MW; 1
                           BEKVVPS1PKELK
                                                       GKPAYLIDTYQDLKQDWLEGIEVVGVTAGASAPEVLVQEVIDQLKAWGGETTSVRENSGI
                                                                                                                                                                                             HAGHPEVEGIMGQYEKCTEGGGIYLVETPEDVRNLKVNNPNDLAYVTQTTLSMTDTKVMV
                                                                                                                                                                                                                                 HQVPDGATVIFSAHGVSQAVRRQAAQRGLKVFDATCPLVTKVHLDVARHCRTGRDMILIG
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                                                                                                                                                                                                                                                                                     MQIVLANPRGFCAGVDRAIBIVDQAIEAFGAPIYVRHEVVHNRTVVDGLKQKGAVFIEBL
                                                                                                               DALRORFPTIQGPKNNDICYATONRODAVRELARECDLVLVVGSPNSSNSNRLSELAORE
                                                                                                                                          DALREQFPSIKEOKKODICYATONRODAVHDLAKISDLILVVGSPNSSNSNRLREIAVQL
                                                                                                                                                                        HAGHPEVEGTMGQWDQERGTGRIYLVENIDDVATLHVAQPHHLAYTTQTTLSVDDTRNII
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                 59.6%; Score 967; DB 1; 61.0%; Pred. No. 1.7e-61;
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e proteome.
1A2E80B9A9BD334A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                               Length 316;
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Search completed: January 29, 2004, 15:50:43
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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3: sp_fungi:*
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Gapop 10.0 , Gapext 0.5
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1623
  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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sp_mhc:*
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Q8det0 vibrio viln
Q8dbr2 viggleswort
Q8dbr2 viggleswort
Q8dgp0 corymebacte
Q8g257 bricella su
Q8g418 bifidobacte
Q8f313 leptospira
Q8i295 plasmodium
Q9bjx6 plasmodium
Q9bjx6 plasmodium
Q9bjx6 plasmodium
Q9bjx6 plasmodium
Q8ri52 fusobacteri
Q8ewr9 mycoplasma
Q97i09 clostridium
Q8dk29 synechococc
Q9fap0 adonis pala
Q94b35 arabidopsis
Q8kfn9 chlorobium
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01-MAR-2003 (TrEMBLrel. 23, Last sec
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Penicillin tolerance protein LytB.
LYTB OR SO3529
Shewanella oneidensis.
Bacteria: Protect
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Heidelberg J.F., Paulsen I.T., Nelson K.E., Galdos E.J., Nelson W.C.,
Heidelberg J.F., Paulsen I.T., Nelson K.E., Galdos E.J., Nelson W.C.,
Read T.D., Sisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
Vamathevan J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
Mueller J., Xhouri H., Gill J., Utterback T.R., McDonald L.A.,
Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
"Genome sequence of the dissimilatory metal ion-reducing bacterium
Shewanella oneidensis.";
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EMBL; AE015789; AAN56520.1; -.
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     EEKVVFSIPKELK 313
                                                          GTQSYLVDTADDIDSSWFENITKVAVTAGASAPEVLVQQVVQAIAKLA--PSVVTEVEGR
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Nat. Genet. 32:402-407(2002).
EMBL; AB063521; BAC24438.1; -.
SEQUENCE FROM N.A.
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A Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,

A Paulsen I.T., Seshadri R., Nelson K.E., Solonay J.F., Madupu R.,

A Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,

A Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,

A Nelson M.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.

A Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,

A Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,

A Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;

T "The Brucella suis genome reveals fundamental similarities between

T animal and plant pathogens and symbionts.";

L Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
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EMBL; AP005217; BAC17889.1; -.
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372 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLG-KPAYLIDTYQDLKQDWLEGIEVVGVTAGASAPEVLVQEVIDQLKAWGGETTSVREN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Trexhirel. 23, Created)
(Trexhirel. 23, Last sequence update)
(Trexhirel. 23, Last annotation updat
*~lerance protein LytB.
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     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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1., Mashima J., Itoh T., Yamagishi A., Nishio
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                           46.3%;
                                                                                                         MW.
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                           Score 751;
Pred. No. :
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Pred. No. 2.3e-49;
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                                                                                                         365B990651BCC9BC
     Mismatches
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                        2.6e-48;
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Best Local
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                                                                                                                                                                                                                                                          Complete proteome. SEQUENCE 352 AA;
                                                                                                                                                                                                                                                                                                                                   MEDLINE=22294977; PubMed=12381787; Schell M.A., Karmirantzou M., Snel Pessi G., Zwahlen M.-C., Desiere F. Pridmore R.D., Arigoni F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAR-2003 (TEMMLIFEL 23, Last sequence update) 01-WAR-2003 (TEMMLIFEL 23, Last annotation update) IspH protein involved in conversion of 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate into
                                                                                                                                                                                                                                                                                   EMBL; AE014766; AAN25161.1; -.
                                                                                                                                                                                                                                                                                               to the human gastrointestinal tract."; Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bifidobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bifidobacterium longum.
Bacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                        167
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                                                                                                                                                                                                                                                                                                                       genome sequence of Bifidobacterium longum
202
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                                                                       AKHAKOGREVILIGHAGHPEVECTMGQYEKCTEGGGIYLVETPEDVRNIKVNNPNDLAYV
SQTTLSVDETADTIAALKAKFPWIQEPPSSDICYATSNRQAAVKLVAQQSDCVVIVGSAN
                     TOTTLSWIDTKVMVDALREOFFSIKEOKKDDICYATONRODAVHDLAKISDLILVVGSPN
                                                  LREVREG
                                                                                                    QGAVFVQELAEIPDAAAQAĞIPVVFSAHGVSPVVKAEAERRGMHVVDATCPLVGKVHREV
                                                                                                                           KGAVFIEELSDVP-----VGSYLIFSAHGVSKEVQQEAEERQLTVFDATCPLVTKVHWQV 106
                                                                                                                                                     VVIADPRGFCAGVDRAILTVQTILKAAEASGKRTREDGLPPVYVRRQIVHNKHVVEDLAG
                                                                                                                                                                     IVLANPRGECAGVDRAI---EIVDQAIEAFG------APIYVRHEVVHNRTVVVDGLKQ
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                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                          37863 MW;
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4; Mismatches
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Q8F3I3;
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                     MEDLINE=22255708; PubMed=12368867; Hall N., Pain A., Berriman M., Chu Mungall K., Bowman S., Atkin R., B
                                                                                                                 Plasmodium faîciparum
Eukaryota; Alveolata;
NCBI_TaxID=36329;
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57; Mismatches
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                     Harris B.,
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A Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
A Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
A Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance
A Hamper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
A Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
A Knights A., Konforttov B., Kyes S., Larke N., Lawson D., Lennard N.
A Knights A., Konforttov B., Kyes S., Larke N., Lawson D., Lennard N.
A Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
A Coliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,
A Rajandream M.A., Rutter S., Rutherford K.M., Sanders K., Simmonds i
Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
A Sulston J.B., Craig A., Newbold C., Barrell B.G;
"Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
PMBI. ALGATAGS. CAPAGOS. 1.
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Q9BJX6;
Q1-JUN-2001
01-JUN-2001
01-MAR-2003
InterPro; IPR003451; LytB.
InterPro; IPR002052; N6 Mtase.
Pfam; PF02401; LYTB; 1.
TIGREAMs; TIGR00216; ispH lytB;
PROSITE; PS00092; N6 MTASE; 1.
                                                                                                                 Beck E., Jomaa H.;

"GCPE Is Involved in the 2-C-Methyl-D-Erythritol 4-Phosphate of Isoprenoid Biosynthesis in Escherichia coli.";

J. Bacteriol. 183:2411-2416(2001).

BMBL; AF322927; AAKLI102.1;

BMBL; AF322927; AAKLI102.1;
                                                                                                                                                                                                                                                                   MEDLINE=21172855; PubMed=11274098; Altincicek B., Kollas A.K., Sanderbrand
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Eukaryota; Alveolata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVVFSIPKELKKHM 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAVLLNTVHDLDQQILKNVNKIALTSAASTPEQETQKFVNLLTNPPFNYTLQNFDGAHEN
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Pred. No. 1.1e-36;
8; Mismatches 120
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                                                                                                                                                                                                                                                                        Wiesner J.,
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lin N., Hance
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InterPro; IPR003451; LytB.
InterPro; IPR003029; S1.
Pfam; PF02401; LYTB; 1.
Pfam; PF00575; S1; 4.
SMART; SM00316; S1; 6.
TIGREAMS; TIGR00216; 1apH lytB; 1.
PROSITE; PS50126; S1; 4.
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OSRI52;
01-JUN-2002 (TIEMBLITEL 2
01-JUN-2002 (TIEMBLITEL 2
01-MAR-2003 (TIEMBLITEL 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Pusobacteria;
Pusobacterium.
NCBI Tavin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC 25586;

MEDLINS=21886394; PubMed=11889109;

Kapatral V. Anderson I., Ivanova N., Reznik G., Los T., Lykidis ;

Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,

Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,

Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,

Fonstein M., Kyrpides N., Overbeek R.;

"Genome sequence and analysis of the oral bacterium Fusobacterium pucleatum strain ATCC 2586.";

D. Bacteriol. 184:2005-2018 (2002).
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----LSDVPVGSYLIFSAHGVSKEVQQBAEERQLTVFDATCPLVTKVHMQVAKHAKQGR 114
                                                                                     MEITRAKHMGFCFGVLBAINVCNSLVEEKGRK-YILGMLVHNKQVVEDMERKGFKLVTED 59
                                                                                                                                                                                                                                                                                                               proteome.
827 AA;
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                                                                                                                                             MQIVLANPRGFCAGVDRAIEIVDQAIEAFGAPIYVRHEVVHNRTVVDGLKQKGAVFIEE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAYLIDTYODLKODWLEGIEVVGVTAGASAPEVLVQEVIDOL
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                                                                                                                                                                                                                                                                                                                  94507 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62504 MW;
                                                                                                                                                                                            24.9%; Score 404.5; DB 16; Length 30.7%; Pred. No. 8.9e-22; tive 68; Mismatches 119; Indels
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43.6%; Pred. No. 1.3e-36;
tive 55; Mismatches 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycoplasma penetrans.
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InterPro; IPR003451; LytB.
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InterPro; IPR003029; S1.
Pfam; PF00401; LYTB; 1.
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SMART; SM00316; S1; 4.
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J. Bacteriol. 183:4823-4838(2001).
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Clostridium acetobutylicum.
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STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
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MEDLINE=20461233; PubMed=11004185; Cunningham F.X. Jr., Lafond T.P., Garantingham F.X., Lafond T.P., Garantingham F.X., Lafond T.P., Garantingham F.X., Lafond T.P., Garantingham F.X., Lafond T.P., Lafond T.P., Lafond T.P., Lafond T.P., Lafond T.P., Lafond T.P., Lafond T.P., Garantingham F.X., Lafond T.P., Lafond T.P., Garantingham F.X., Lafond T.P., Lafond T

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Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                 SEQUENCE FROM N.A.

SOUTHWICK A., KARIIN-Neumann G., Nguyen M., Lam B., Miranda M., Southwick A., Kariin-Neumann G., Banh J., Carninci P., Chen H., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Bcker J., Theologis A., Davis R.W.;

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
Submitted [3]
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Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
Palm C.J., Bewser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Ecker J., Theologis A., Davis R.W.,
Ecker J., Theologis A., Davis R.W.,
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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Pfam; PF02401; LYTB; 1.
TIGRFAMS; TIGR00216; ispH_lytB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKGEYTSIIHGKYSHEETIAT-----ASFAGKYII------VKNMDEAMYVCDY
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52112 MW;
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; 702D1F0ED3669D45 CRC64;
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Best Local S
Matches 98
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"The Arabidopsis IspH (LytB) homolog: Its role in chloroplast development and maintenance of thylakoid membranes.";

Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

R EMBL; AY042877; AAK68817.1; -.

REMBL; AY081454; AAM10016.1; -.

REMBL; AY168881; AAN87171.1; -.

R EMBL; AY168881; AAN87171.1; -.

R InterPro; IPR003451; LytB.

R InterPro; IPR003451; LytB.

R TIGRPAMS; TIGRO216; ispH_lytB; 1.

Hypothetical protein.

SQUENCE 466 AA; 52781 MW; B008808517890DC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
   39E
                                  244
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                                                                                                                                                                                                                                                                                                                                                                                                                            98;
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SYWIDSEKRIGPGNKIAYKLHYGELVEKENFLPKGPITIGVTSGASTPDKVVEDAL
                                                                                                                                                                                                                                                                                                                                                    VKLAKAYGPCWGVERAVQIAYBARKQPPEBRLWIINEIIHNPTVNKRLEDMDVKIIPVED
                                    AYLIDT--
                                                                     CHFISE ----
                                                                                        EQFPSIKEQKKDDICYATQNRQDAVHDLAKIS-DLILVVGSPNSSNSNRLREIAVQLGKP
                                                                                                                                                                                                            SVIHGKYNHEETIAT----ASFAGKYII-----VKNMKBANYVCDYILGGQYDGSSS
                                                                                                                                                                                                                                             VILIGHAGHPEVEGTMGQYEKCTEGGGIYLVETPEDVRNLKVNN-------
                                                                                                                                                                                                                                                                                  SKKQFDVVEKDDVVILPÅFGAGVDEMYVLNDKKVQIVDTTCPWVTKVMNTVEKHKKGEYT 232
                                                                                                                                                                                                                                                                                                                 --EBLSDVPVGSYLIFSAHGVSKEVQQEABERQLTVFDATCPLVTKVHMQVAKHAKQGRE 115
                                                                                                                                         TKEBFMEKFKYAISKGFDPDNDLVKVGIANQTTMLKGETEBIGRLLETTMMRKYGVENVS
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                                                                  -NTICDATQERQDAIYELVEEKIDLMLVVGGWNSSNTSHLQEISEARGIP
                                                                                                                                                                                                                                                                                                                                                                                                                          18.5%; Score 300; DB 10; 27.5%; Pred. No. 2.8e-14; tive 56; Mismatches 108;
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                    YQDL--KQDWL-EGIEVVGVTAGASAPEVLVQEVI
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Search completed: January 29, 2004, 15:54:14 Job time: 25.7034 secs